STIC Search Report
Biotech-Chem Library

STIC Database Tracking Number: 120495

TO: Bao-thuy Nguyen Location: REM-3D51/3C70 Art Unit: 1641 Wednesday, April 28, 2004 Case Serial Number: 09/845729	From: Barb O'Bryen Location: Biotech-Chem Library Remsen 1A69 Phone: 571-272-2518 BOB barbara.obryen@uspto.gov

Search Notes

RUSH

120495

STIC-Biotech/ChemLib

From: Chan, Christina
Sent: Tuesday, April 27, 2004 1:58 PM
To: Nguyen, Bao-Thuy; STIC-Biotech/ChemLib
Subject: RE: 09/845,729

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

-----Original Message-----
Fr m: Nguyen, Bao-Thuy
Sent: Tuesday, April 27, 2004 12:44 PM
To: Chan, Christina
Subject: 09/845,729

Chris:

Please approve a rush search for 09/845,729. It is an overdue amendment that was reassigned to me yesterday. Thank You.

STIC-BIOTECH: Please search residues 2-14 of SEQ ID No. 1.

Thank You
Bao-Thuy Nguyen
AU 1641
(571) 272-0824
Remsen 3D51
Mailbox 3C70

Searcher:_____
Phone:_____
Location:_____
Date Picked Up:_____
Date Completed:_____
Searcher Prep/Review:_____
Clerical:_____
Online time:_____

TYPE OF SEARCH:
NA Sequences:_____
AA Sequences:_____
Structures:_____
Bibliographic:_____
Litigation:_____
Full text:_____
Patent Family:_____
Other:_____

VENDOR/COST (where applic.)
STN:_____
DIALOG:_____
Questel/Orbit:_____
DRLink:_____
Lexis/Nexis:_____
Sequence Sys.:_____
WWW/Internet:_____
Other (specify):_____

OM protein - protein search, using sw model

Run on: April 27, 2004, 16:22:48 ; Search time 21 Seconds
(without alignments)
59.547 Million cell updates/sec

Title: US-09-845-729A-1_COPY_2_14
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	61	93.8	16	2	H29501	fibrinopeptide A -
2	57	87.7	16	2	C28854	fibrinopeptide A -
3	57	87.7	16	2	A24180	fibrinogen alpha c
4	57	87.7	16	2	B24180	fibrinogen alpha c
5	57	87.7	16	2	A28854	fibrinopeptide A -
6	57	87.7	16	2	B28854	fibrinopeptide A -
7	57	87.7	16	2	A29501	fibrinopeptide A -
8	57	87.7	644	1	FGHUA	fibrinogen alpha c
9	57	87.7	866	2	D44234	fibrinogen alpha c
10	52	80.0	15	2	F29501	fibrinopeptide A -
11	51	78.5	16	2	G29501	fibrinopeptide A -
12	51	78.5	28	2	A05296	fibrinogen alpha c
13	49	75.4	17	2	E29501	fibrinopeptide A -
14	48	73.8	15	2	I29501	fibrinopeptide A -
15	48	73.8	19	2	B29501	fibrinopeptide A -
16	48	73.8	19	2	C29501	fibrinopeptide A -
17	48	73.8	311	2	A05294	fibrinogen alpha c
18	40	61.5	15	2	JP0101	fibrinogen alpha c
19	40	61.5	280	2	H89800	hypothetical prote
20	39	60.0	236	2	S48867	dimethylallyltrans
21	39	60.0	245	2	AG0701	Orf 245 protein [i
22	39	60.0	271	2	S18730	aminoglycoside N3'
23	39	60.0	324	2	D70943	hypothetical prote
24	39	60.0	705	2	T31157	hypothetical prote
25	38.5	59.2	732	2	AB2732	conserved hypothet
26	38.5	59.2	741	2	B97513	probable secreted
27	38	58.5	575	2	T48224	probable homeodoma
28	38	58.5	611	1	S12566	translation initia
29	38	58.5	652	2	AD2316	hypothetical prote
30	38	58.5	669	2	A72718	hypothetical prote
31	38	58.5	686	2	T08919	hypothetical prote
32	38	58.5	727	2	T08920	hypothetical prote
33	38	58.5	742	2	T00371	hypothetical prote
34	37	56.9	149	2	G85534	hypothetical prote
35	37	56.9	149	2	C90684	hypothetical prote
36	37	56.9	164	2	E70639	hypothetical prote
37	37	56.9	302	2	F90526	hypothetical prote
38	37	56.9	363	2	G71544	hypothetical prote
39	37	56.9	410	2	F96683	hypothetical prote
40	37	56.9	412	2	S28423	isocitrate dehydro
41	37	56.9	415	2	S65065	isocitrate dehydro
42	37	56.9	416	2	S47013	isocitrate dehydro
43	37	56.9	416	2	A96585	NADP specific isoc
44	37	56.9	421	2	D69643	imidazolone-5-prop
45	37	56.9	433	2	T09619	isocitrate dehydro

ALIGNMENTS

RESULT 1
H29501
fibrinopeptide A - gray seal
C;Species: Halichoerus grypus (gray seal)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C;Accession: H29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serc
A;Reference number: A29501
A;Accession: H29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfic

Query Match 93.8%; Score 61; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          2 ESDFLAEGGGVR 13
              ||||||||||||
Db          5 ESDFLAEGGGVR 16
```

RESULT 2
C28854
fibrinopeptide A - gelada baboon
C;Species: Theropithecus gelada (gelada baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: C28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropith
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: C28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 ESDFLAEGGGVR 13
              | ||||||||||
Db          5 EGDFLAEGGGVR 16
```

RESULT 3
A24180
fibrinogen alpha chain - Japanese macaque (fragment)
N;Contains: fibrinopeptide A

C;Species: Macaca fuscata (Japanese macaque)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 26-Jan-1996
C;Accession: A24180
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E
uenons, and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Accession: A24180
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 4
B24180
fibrinogen alpha chain - red guenon (fragment)
N;Contains: fibrinopeptide A
C;Species: Erythrocebus patas (red guenon, hussar)
C;Date: 05-Jun-1988 #sequence_revision 10-Mar-1994 #text_change 26-Jan-1996
C;Accession: B24180
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 97, 1487-1492, 1985
A;Title: Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and patas monkey (E
uenons, and baboons.
A;Reference number: A91990; MUID:85289140; PMID:3928610
A;Accession: B24180
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 5
A28854
fibrinopeptide A - olive baboon
C;Species: Papio anubis, Papio hamadryas anubis (olive baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: A28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropit
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: A28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 6
B28854
fibrinopeptide A - hamadryas baboon
C;Species: Papio hamadryas (hamadryas baboon)
C;Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 26-Jan-1996
C;Accession: B28854
R;Nakamura, S.; Takenaka, O.; Takahashi, K.
J. Biochem. 94, 1973-1978, 1983
A;Title: Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas, and Theropith
A;Reference number: A91973; MUID:84161822; PMID:6423621
A;Accession: B28854
A;Molecule type: protein
A;Residues: 1-16 <NAK>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 7
A29501
fibrinopeptide A - baboon
C;Species: Papio sp. (baboon)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 26-Jan-1996
C;Accession: A29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serc
A;Reference number: A29501
A;Accession: A29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.00076;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGDFLAEGGGVR 16

RESULT 8
FGHUA
fibrinogen alpha chain precursor, short splice form [validated] - human
N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 30-Jun-1987 #text_change 08-Dec-2000
C;Accession: A93956; A43568; A90468; I84456; A44234; C44234; B94433; A90433; B94309; S192
R;Kant, J.A.; Lord, S.T.; Crabtree, G.R.
Proc. Natl. Acad. Sci. U.S.A. 80, 3953-3957, 1983
A;Title: Partial mRNA sequences for human Aalpha, Bbeta, and gamma fibrinogen chains: evc
A;Reference number: A93956; MUID:83247396; PMID:6575389
A;Accession: A93956
A;Molecule type: mRNA
A;Residues: 1-644 <KAN>
A;Cross-references: GB:J00128; NID:g182425; PIDN:AAA52427.1; PID:g182426
A;Note: the authors translated the codon GAG for residue 247 as Gly, GGA for residue 438
R;Chung, D.W.; Harris, J.E.; Davie, E.W.
Adv. Exp. Med. Biol. 281, 39-48, 1990
A;Title: Nucleotide sequences of the three genes coding for human fibrinogen.
A;Reference number: A43568; MUID:91344740; PMID:2102623
A;Accession: A43568
A;Molecule type: DNA
A;Residues: 1-330,'A',332-644 <CHU>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
R;Rixon, M.W.; Chan, W.Y.; Davie, E.W.; Chung, D.W.

Biochemistry 22, 3237-3244, 1983
A;Title: Characterization of a complementary deoxyribonucleic acid coding for the alpha
A;Reference number: A90468; MUID:83283432; PMID:6688355
A;Accession: A90468
A;Molecule type: mRNA
A;Residues: 1-330,'A',332-629 <RIX>
A;Cross-references: GB:J00127; NID:g182423; PIDN:AAA52426.1; PID:g182424
R;Imam, A.M.A.; Eaton, M.A.W.; Williamson, R.; Humphries, S.
Nucleic Acids Res. 11, 7427-7434, 1983
A;Title: Isolation and characterisation of cDNA clones for the Aalpha- and gamma-chains
A;Reference number: I37393; MUID:84069777; PMID:6689067
A;Accession: I84456
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 110-156 <RES>
A;Cross-references: GB:K02272; NID:g182427; PIDN:AAA52428.1; PID:g182428
R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
A;Reference number: A44234; MUID:93090725; PMID:1457396
A;Accession: A44234
A;Molecule type: mRNA
A;Residues: 1-51 <FU1>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A;Note: sequence extracted from NCBI backbone (NCBIN:119912, NCBIN:119914, NCBIP:119918)
A;Accession: C44234
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 605-644 <FU2>
A;Cross-references: GB:M64982; NID:g458553; PIDN:AAA17055.1; PID:g458554
A;Note: sequence extracted from NCBI backbone (NCBIP:119920)
R;Henschen, A.; Lottspeich, F.; Southan, C.; Topfer-Petersen, E.
in Protides of the Biological Fluids, Proc. 28th Colloq., Peeters, H., ed., pp.51-56, Pe
A;Title: Human fibrinogen: sequence, sulfur bridges, glycosylation and some structural v
A;Reference number: A94433
A;Accession: B94433
A;Molecule type: protein
A;Residues: 20-214,'RS',217-298,'G',300-303,'G',305-629 <HEN>
R;Watt, K.W.K.; Cottrell, B.A.; Strong, D.D.; Doolittle, R.F.
Biochemistry 18, 5410-5416, 1979
A;Title: Amino acid sequences studies on the alpha chain of human fibrinogen. Overlappin
A;Reference number: A90433; MUID:80088231; PMID:518846
A;Contents: disulfide bonds
A;Accession: A90433
A;Molecule type: protein
A;Residues: 20-146,'Q',148-195,'N',197-230,'N',232-316,'SG',319-406,'D',408,'N',410-629
R;Blomback, B.; Hessel, B.; Hogg, D.
Thromb. Res. 8, 639-658, 1976
A;Title: Disulfide bridges in NH-2-terminal part of human fibrinogen.
A;Reference number: A94309; MUID:76225080; PMID:936108
A;Contents: variant, and disulfide bonds
A;Accession: B94309
A;Molecule type: protein
A;Residues: 20-65,'T',67-629 <BLO>
R;Dewey, R.S.; Liesch, J.M.; Williams, H.R.; Sugg, E.E.; Dolan, C.A.; Davies, P.; Mumfor
Biochem. J. 281, 519-524, 1992
A;Title: Purification and characterization by fast-atom-bombardment mass spectrometry of
incubation with calcium ionophore A23187.
A;Reference number: S19297; MUID:92143822; PMID:1736899
A;Accession: S19297
A;Molecule type: protein
A;Residues: 20-40 <DEW>
R;Retzios, A.D.; Markland Jr., F.S.
Thromb. Res. 52, 541-552, 1988
A;Title: A direct-acting fibrinolytic enzyme from the venom of Agkistrodon contortrix co
A;Reference number: A60905; MUID:89162316; PMID:3232124
A;Accession: A60905
A;Molecule type: protein
A;Residues: 433-451 <RET>
R;Fretto, L.J.; Ferguson, E.W.; Steinman, H.M.; McKee, P.A.
J. Biol. Chem. 253, 2184-2195, 1978
A;Title: Localization of the alpha-chain cross-link acceptor sites of human fibrin.
A;Reference number: A92225; MUID:78130085; PMID:632262
A;Contents: annotation; cross-linking acceptor sites
R;Cottrell, B.A.; Strong, D.D.; Watt, K.W.K.; Doolittle, R.F.
Biochemistry 18, 5405-5410, 1979
A;Title: Amino acid sequence studies on the alpha chain of human fibrinogen. Exact locati
A;Reference number: A90432; MUID:80088230; PMID:518845
A;Contents: annotation; cross-linking acceptor sites
R;Henschen, A.; Lottspeich, F.; Kehl, M.; Southan, C.
Ann. N. Y. Acad. Sci. 408, 28-43, 1983
A;Title: Covalent structure of fibrinogen.
A;Reference number: A90037; MUID:83254370; PMID:6575689
A;Contents: annotation; review, disulfide bonds
R;Itarte, E.; Plana, M.; Guasch, M.D.; Martos, C.
Biochem. Biophys. Res. Commun. 117, 631-636, 1983
A;Title: Phosphorylation of fibrinogen by casein kinase 1.
A;Reference number: A90116; MUID:84104274; PMID:6318767
A;Contents: annotation; phosphorylation
A;Note: about one-third of alpha chain molecules in blood were found to be phosphorylatec
R;Doolittle, R.F.
Annu. Rev. Biochem. 53, 195-229, 1984
A;Title: Fibrinogen and fibrin.
A;Reference number: A90041; MUID:84305751; PMID:6383194
A;Contents: annotation; review, EM structure, polymerization, ligands
R;Kimura, S.; Aoki, N.
J. Biol. Chem. 261, 15591-15595, 1986
A;Title: Cross-linking site in fibrinogen for alpha-2-plasmin inhibitor.
A;Reference number: A92565; MUID:87057190; PMID:2877981
A;Contents: annotation; cross-linking site for alpha-2-plasmin inhibitor
R;Krishnamurthi, S.; Dickens, T.A.; Patel, Y.; Wheeler-Jones, C.P.D.; Kakkar, V.V.
Biochem. Biophys. Res. Commun. 163, 1256-1264, 1989
A;Title: The fibrinogen-derived peptide (RGDS) prevents proteolytic degradation of protei
A;Reference number: A33261; MUID:89392031; PMID:2783136
A;Contents: annotation; activity of cell attachment (R-G-D) motif
R;Kirschbaum, N.E.; Budzynski, A.Z.
J. Biol. Chem. 265, 13669-13676, 1990
A;Title: A unique proteolytic fragment of human fibrinogen containing the Aalpha COOH-te
A;Reference number: A37117; MUID:90337977; PMID:2143188
A;Contents: annotation; hementin cleavage site
A;Note: hementin, a protease from Haementeria ghilianii, the giant South American leech,
R;Staendker, L.; Sillard, R.; Bensch, K.W.; Ruf, A.; Raida, M.; Schulz-Knappe, P.; Schepk
Biochem. Biophys. Res. Commun. 215, 896-902, 1995
A;Title: In vivo degradation of human fibrinogen A alpha: Detection of cleavage sites and
A;Reference number: JC4334; MUID:96027996; PMID:7488058
A;Contents: annotation; composition and amino-terminal sequences of carboxyl end peptides
C;Comment: Unlike the beta and gamma chains, the alpha chain is not glycosylated.
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleaves
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:D44234 for the minor alternative splice form.
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMIM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of alpha, beta (see I
ins are contained in the core. Two three-chain coiled coils emerge from this core and cor
from the distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into f
A;Pathway: blood coagulation
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C;Keywords: alternative splicing; blood coagulation; coiled coil; glycoprotein; liver; ph
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-629/Product: fibrinogen alpha chain #status experimental <MAT>
F;20-35/Product: fibrinopeptide A #status experimental <APT>
F;36-629/Product: fibrin alpha chain #status experimental <FGA>
F;36-38/Region: polymerization site, binding to the distal domain of the gamma chain of a
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental

```
F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
F;55/Disulfide bonds: interchain (to beta-95) #status experimental
F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
F;68/Disulfide bonds: interchain (to beta-106) #status experimental
F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
F;184/Disulfide bonds: interchain (to beta-223) #status experimental
F;288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F;322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #
F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status exp
F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status

  Query Match             87.7%;  Score 57;  DB 1;  Length 644;
  Best Local Similarity   91.7%;  Pred. No. 0.039;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | ||||||||||
Db         24 EGDFLAEGGGVR 35


RESULT 9
D44234
fibrinogen alpha chain precursor, extended splice form - human
N;Alternate names: coagulation factor I
N;Contains: fibrinopeptide A
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1993 #sequence_revision 06-Sep-1996 #text_change 19-Jan-2001
C;Accession: D44234; B44234
R;Fu, Y.; Weissbach, L.; Plant, P.W.; Oddoux, C.; Cao, Y.; Liang, T.J.; Roy, S.N.; Redma
Biochemistry 31, 11968-11972, 1992
A;Title: Carboxy-terminal-extended variant of the human fibrinogen alpha subunit: a nove
A;Reference number: A44234; MUID:93090725; PMID:1457396
A;Accession: D44234
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA; DNA
A;Residues: 1-866 <FU1>
A;Cross-references: GB:M58569; NID:g182406; PID:g182407
A;Note: neither the complete nucleic acid sequence nor the complete translation are show
A;Accession: B44234
A;Molecule type: mRNA; DNA
A;Residues: 605-866 <FU2>
A;Note: sequence extracted from NCBI backbone (NCBIP:119917)
C;Comment: The alpha chain binds by 2-4 cross-links to the amino end of fibronectin.
C;Comment: The conversion of fibrinogen to fibrin is triggered by thrombin, which cleave
ization sites responsible for the formation of the soft clot.
C;Comment: The soft clot is converted into the hard clot by factor XIIIa (fibrin-stabili
ger) and between alpha chains (weaker) of different monomers.
C;Comment: All fibrinogen chains are synthesized in the liver.
C;Comment: See PIR:FGHUA for the major splice form. It is not known whether this form is
C;Genetics:
A;Gene: GDB:FGA
A;Cross-references: GDB:119129; OMIM:134820
A;Map position: 4q28-4q28
A;Introns: 18/3; 60/3; 122/1; 171/2
A;Note: the list of introns is incomplete
C;Complex: The fibrinogen molecule is a hexamer containing two sets of three nonidentica
ntained in the core. Two three-chain coiled coils emerge from this core and connect it t
distal domain nodes.
C;Function:
A;Description: fibrinogen cleaved by thrombin yields monomers that are polymerized into
A;Pathway: blood coagulation
C;Superfamily: human extended splice form fibrinogen alpha chain; fibrinogen beta/gamma
C;Keywords: alternative splicing; blood coagulation; glycoprotein; liver; phosphoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-863/Product: fibrinogen alpha chain, extended splice form #status predicted <MAT>
F;20-35/Product: fibrinopeptide A #status experimental <APT>
F;36-863/Product: fibrin alpha chain, extended splice form #status predicted <FGA>
F;57-185/Domain: fibrinogen disulfide ring homology <FDR>
F;591-593/Region: cell attachment (R-G-D) motif
F;629-863/Domain: fibrinogen beta/gamma homology <FBG>
F;22,460/Binding site: phosphate (Ser) (covalent) #status experimental
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```
F;35-36/Cleavage site: Arg-Gly (thrombin) #status experimental
F;47/Disulfide bonds: interchain (to alpha-47) #status experimental
F;55/Disulfide bonds: interchain (to beta-95) #status experimental
F;64/Disulfide bonds: interchain (to gamma-49) #status experimental
F;68/Disulfide bonds: interchain (to beta-106) #status experimental
F;180/Disulfide bonds: interchain (to gamma-165) #status experimental
F;184/Disulfide bonds: interchain (to beta-223) #status experimental
F;288,419/Binding site: carbohydrate (Asn) (covalent) #status absent
F;322/Cross-link: isopeptide (Lys) (interchain to Gln-41 of alpha-2-plasmin inhibitor) #s
F;347,385/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of alpha) #status expe
F;461-491/Disulfide bonds: #status experimental
F;527,558,575,581,599/Cross-link: isopeptide (Lys) (interchain to Gln of alpha) #status p
F;686,831/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             87.7%;  Score 57;  DB 2;  Length 866;
  Best Local Similarity   91.7%;  Pred. No. 0.053;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | ||||||||||
Db         24 EGDFLAEGGGVR 35


RESULT 10
F29501
fibrinopeptide A - wombat
C;Species: Vombatidae gen. sp. (wombat)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C;Accession: F29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serc
A;Reference number: A29501
A;Accession: F29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

  Query Match             80.0%;  Score 52;  DB 2;  Length 15;
  Best Local Similarity   76.9%;  Pred. No. 0.0055;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              :|  |||||||||
Db          3 TEGSFLAEGGGVR 15


RESULT 11
G29501
fibrinopeptide A - bear
C;Species: Ursus sp. (bear)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C;Accession: G29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serc
A;Reference number: A29501
A;Accession: G29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-16 <BLO>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfic

  Query Match             78.5%;  Score 51;  DB 2;  Length 16;
  Best Local Similarity   75.0%;  Pred. No. 0.0089;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | :|:|||||||
Db          5 EGEFIAEGGGVR 16


RESULT 12
A05296
```

fibrinogen alpha chain - dog (fragment)
C;Species: Canis lupus familiaris (dog)
C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 25-Oct-1996
C;Accession: A94308; A03118; A37511; A05296; B37511; C03118
R;Birken, S.; Wilner, G.D.; Canfield, R.E.
Thromb. Res. 7, 599-610, 1975
A;Title: Studies of the structure of canine fibrinogen.
A;Reference number: A94308; MUID:76081726; PMID:1198547
A;Accession: A94308
A;Molecule type: protein
A;Residues: 1-28 <BIR>
R;Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A;Title: Studies on fibrinopeptides from mammals.
A;Reference number: A03118
A;Accession: A03118
A;Molecule type: protein
A;Residues: 1-16 <BLO>
R;Osbahr Jr., A.J.; Colman, R.W.; Laki, K.; Gladner, J.A.
Biochem. Biophys. Res. Commun. 14, 555-558, 1964
A;Reference number: A37511; MUID:66020594; PMID:5836555
A;Accession: A37511
A;Molecule type: protein
A;Residues: 1,'D',3,'EGKQ',8-16 <OSB>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C;Keywords: blood coagulation; liver; phosphoprotein; plasma
F;1-16/Product: fibrinopeptide A #status experimental <APT>
F;3/Binding site: phosphate (Ser) (covalent) (partial) #status experimental

  Query Match 78.5%; Score 51; DB 2; Length 28;
  Best Local Similarity 75.0%; Pred. No. 0.016;
  Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 5 EGEFIAEGGGVR 16

RESULT 13
E29501
fibrinopeptide A - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C;Accession: E29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Ser
A;Reference number: A29501
A;Accession: E29501
A;Molecule type: protein
A;Residues: 1-17 <BLO>
R;Blombaeck, B.; Blombaeck, M.; Groendahl, N.J.
Acta Chem. Scand. 19, 1789-1791, 1965
A;Title: Studies on fibrinopeptides from mammals.
A;Reference number: A03118
A;Contents: annotation; confirmation of species assignment
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfi

  Query Match 75.4%; Score 49; DB 2; Length 17;
  Best Local Similarity 75.0%; Pred. No. 0.022;
  Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 6 KGEFLAEGGGVR 17

RESULT 14
I29501
fibrinopeptide A - kangaroo
C;Species: Macropus sp. (kangaroo)
C;Date: 21-Nov-1987 #sequence_revision 08-Jun-1990 #text_change 18-Aug-2000
C;Accession: I29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serc
A;Reference number: A29501
A;Accession: I29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <BLO>
C;Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology

  Query Match 73.8%; Score 48; DB 2; Length 15;
  Best Local Similarity 75.0%; Pred. No. 0.029;
  Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
Db 4 EGTFIAEGGGVR 15

RESULT 15
B29501
fibrinopeptide A - European moose
C;Species: Alces alces alces (European moose, elk)
C;Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 18-Aug-2000
C;Accession: B29501
R;Blombaeck, B.; Blombaeck, M.; Hann, C.
unpublished results, cited by Blombaeck, B., and Blombaeck, M., in Chemotaxonomy and Serc
A;Reference number: A29501
A;Accession: B29501
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-19 <BLO>
C;Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfic

  Query Match 73.8%; Score 48; DB 2; Length 19;
  Best Local Similarity 90.0%; Pred. No. 0.037;
  Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DFLAEGGGVR 13
Db 10 EFLAEGGGVR 19

Search completed: April 27, 2004, 16:24:55
Job time : 22 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2004, 16:22:47 ; Search time 11 Seconds
(without alignments)
61.537 Million cell updates/sec

Title: US-09-845-729A-1_COPY_2_14
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	87.7	16	1	FIBA_MACFU	P12803 macaca fusc
2	57	87.7	19	1	FIBA_CEREL	P14446 cervus elap
3	57	87.7	866	1	FIBA_HUMAN	P02671 homo sapien
4	56	86.2	16	1	FIBA_CERSI	P14535 ceratotheri
5	54	83.1	16	1	FIBA_TAPTE	P14536 tapirus ter
6	53	81.5	16	1	FIBA_HYLLA	P14453 hylobates l
7	53	81.5	18	1	FIBA_CAMDR	P14444 camelus dro
8	53	81.5	19	1	FIBA_BISBO	P14441 bison bonas
9	53	81.5	19	1	FIBA_CERNI	P14447 cervus nipp
10	51	78.5	16	1	FIBA_FELCA	P14450 felis silve
11	51	78.5	28	1	FIBA_CANFA	P02673 canis famil
12	49	75.4	17	1	FIBA_PIG	P14460 sus scrofa
13	49	75.4	18	1	FIBA_LAMGL	P14454 lama glama
14	48	73.8	15	1	FIBA_SYNCA	P14463 syncerus ca
15	48	73.8	16	1	FIBA_EQUAS	P14449 equus asinu
16	48	73.8	16	1	FIBA_MANLE	P14455 mandrillus
17	48	73.8	16	1	FIBA_ODOHE	P14459 odocoileus
18	48	73.8	19	1	FIBA_BUBBU	P14442 bubalus bub
19	48	73.8	19	1	FIBA_SHEEP	P14451 ovis aries
20	48	73.8	596	1	FIBA_BOVIN	P02672 bos taurus
21	47	72.3	14	1	FIBA_HORSE	P14452 equus cabal
22	45	69.2	19	1	FIBA_MUNMU	P14457 muntiacus m
23	41	63.1	271	1	PANB_XANAC	Q8p1l1 xanthomonas
24	41	63.1	271	1	PANB_XANCP	Q8p9t0 xanthomonas
25	40	61.5	15	1	FIBA_ANAPL	P12801 anas platyr
26	40	61.5	1696	1	PCK5_BRACL	Q9nj15 branchiosto
27	39	60.0	13	1	FIBA_CAVPO	P14445 cavia porce
28	39	60.0	236	1	IPT_PANAY	Q47851 pantoea agg
29	39	60.0	271	1	AAC3_PSEAE	P29808 pseudomonas
30	38	58.5	611	1	IF4B_HUMAN	P23588 homo sapien
31	38	58.5	717	1	U84B_HUMAN	Q9uh99 homo sapien
32	37	56.9	19	1	FIBA_RANTA	P14462 rangifer ta
33	37	56.9	413	1	IDHC_SOYBN	Q06197 glycine max
34	37	56.9	415	1	IDHC_TOBAC	P50218 nicotiana t
35	37	56.9	416	1	IDHC_SOLTU	P50217 solanum tub
36	37	56.9	421	1	HUTI_BACSU	P42084 bacillus su
37	37	56.9	421	1	HUTI_STRP3	Q8k5m2 streptococc
38	37	56.9	421	1	HUTI_STRP8	Q8nz53 streptococc
39	37	56.9	421	1	HUTI_STRPY	P58080 streptococc
40	37	56.9	433	1	IDHP_MEDSA	Q40345 medicago sa
41	37	56.9	576	1	PHFF_HUMAN	Q9nqc1 homo sapien
42	36	55.4	16	1	FIBA_MUSVI	P14458 mustela vis
43	36	55.4	220	1	RR3_PSINU	Q8why4 psilotum nu
44	36	55.4	272	1	PANB_XYLFA	Q9pgr9 xylella fas
45	36	55.4	272	1	PANB_XYLFT	Q87ew0 xylella fas

ALIGNMENTS

RESULT 1
FIBA_MACFU
ID FIBA_MACFU STANDARD; PRT; 16 AA.
AC P12803;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN FGA.
OS Macaca fuscata fuscata (Japanese macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey),
OS Macaca mulatta (Rhesus macaque),
OS Cercopithecus aethiops (Green monkey) (Grivet),
OS Erythrocebus patas (Red guenon) (Hussar),
OS Papio anubis (Olive baboon),
OS Papio hamadryas (Hamadryas baboon), and
OS Theropithecus gelada (Gelada baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9543, 9541, 9544, 9534, 9538, 9555, 9557, 9565;
RN [1]
RP SEQUENCE.
RC SPECIES=E.patas, and M.fuscata;
RX MEDLINE=85289140; PubMed=3928610;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of Japanese monkey (Macaca fuscata) and
RT patas monkey (Erythrocebus patas): their amino acid sequences,
RT restricted mutations, and a molecular phylogeny for macaques,
RT guenons, and baboons.";
RL J. Biochem. 97:1487-1492(1985).
RN [2]
RP SEQUENCE.
RC SPECIES=P.anubis, P.hamadryas, and T.gelada;
RX MEDLINE=84161822; PubMed=6423621;
RA Nakamura S., Takenaka O., Takahashi K.;
RT "Fibrinopeptides A and B of baboons (Papio anubis, Papio hamadryas,
RT and Theropithecus gelada): their amino acid sequences and
RT evolutionary rates and a molecular phylogeny for the baboons.";
RL J. Biochem. 94:1973-1978(1983).
RN [3]
RP SEQUENCE.
RC SPECIES=C.aethiops, M.mulatta, and M.fascicularis;
RA Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT "Studies on fibrinopeptides from primates.";
RL Acta Chem. Scand. 19:1788-1789(1965).
CC -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
DR PIR; A24180; A24180.

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DR   PIR; A28854; A28854.
DR   PIR; B24180; B24180.
DR   PIR; B28854; B28854.
DR   PIR; C28854; C28854.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1551 MW;  49E8CBB63EA04DD3 CRC64;

  Query Match             87.7%;  Score 57;  DB 1;  Length 16;
  Best Local Similarity   91.7%;  Pred. No. 0.00075;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | ||||||||||
Db          5 EGDFLAEGGGVR 16


RESULT 2
FIBA_CEREL
ID   FIBA_CEREL     STANDARD;      PRT;    19 AA.
AC   P14446;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Cervus elaphus (Red deer), and
OS   Cervus elaphus nelsoni (American elk).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860, 9864;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=C.elaphus;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=C.e.nelsoni;
RA   Mross G.A., Doolittle R.F.;
RT   "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL   Arch. Biochem. Biophys. 122:674-684(1967).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     19       FIBRINOPEPTIDE A.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  1808 MW;  9BA54C26873B59C5 CRC64;

  Query Match             87.7%;  Score 57;  DB 1;  Length 19;
  Best Local Similarity   84.6%;  Pred. No. 0.00088;
  Matches   11;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              : ||||||||||
Db          7 ASSDFLAEGGGVR 19


RESULT 3
FIBA_HUMAN
ID   FIBA_HUMAN     STANDARD;      PRT;   866 AA.
AC   P02671; Q9BX62; Q9UCH2;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A].
GN   FGA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
RX   MEDLINE=93090725; PubMed=1457396;
RA   Fu Y., Weissbach L., Plant P.W., Oddoux C., Cao Y., Liang T.J.,
RA   Roy S.N., Redman C.M., Grieninger G.;
RT   "Carboxy-terminal-extended variant of the human fibrinogen alpha
RT   subunit: a novel exon conferring marked homology to beta and gamma
RT   subunits.";
RL   Biochemistry 31:11968-11972(1992).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM ALPHA-E).
RA   Chung D.W., Grieninger G.;
RT   "Fibrinogen DNA and protein sequences.";
RL   (In) Ebert R.F. (eds.);
RL   Index of variant human fibrinogens, pp.13-24, CRC Press,
RL   Boca Raton (1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ALPHA-E; ALPHA), AND VARIANTS VAL-6; ALA-331 AND
RP   ALA-456.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 1-655 FROM N.A. (ISOFORM ALPHA-E).
RC   TISSUE=Liver;
RX   MEDLINE=91344740; PubMed=2102623;
RA   Chung D.W., Harris J.E., Davie E.W.;
RT   "Nucleotide sequences of the three genes coding for human
RT   fibrinogen.";
RL   Adv. Exp. Med. Biol. 281:39-48(1990).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX   MEDLINE=83247396; PubMed=6575389;
RA   Kant J.A., Lord S.T., Crabtree G.R.;
RT   "Partial mRNA sequences for human A alpha, B beta, and gamma
RT   fibrinogen chains: evolutionary and functional implications.";
RL   Proc. Natl. Acad. Sci. U.S.A. 80:3953-3957(1983).
RN   [6]
RP   SEQUENCE OF 1-629 FROM N.A.
RX   MEDLINE=83283432; PubMed=6688355;
RA   Rixon M.W., Chan W.-Y., Davie E.W., Chung D.W.;
RT   "Characterization of a complementary deoxyribonucleic acid coding for
RT   the alpha chain of human fibrinogen.";
RL   Biochemistry 22:3237-3244(1983).
RN   [7]
RP   SEQUENCE OF 20-629.
RA   Henschen A., Lottspeich F., Southan C., Topfer-Petersen E.;
RT   "Human fibrinogen: sequence, sulfur bridges, glycosylation and some
RT   structural variants.";
RL   (In) Peeters H. (eds.);
RL   Protides of the biological fluids, Proc. 28th colloquium, pp.51-56,
RL   Pergamon Press, Oxford (1980).
RN   [8]
RP   SEQUENCE OF 20-629, AND DISULFIDE BONDS.
RX   MEDLINE=80088231; PubMed=518846;
RA   Watt K.W.K., Cottrell B.A., Strong D.D., Doolittle R.F.;
RT   "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT   Overlapping sequences providing the complete sequence.";
RL   Biochemistry 18:5410-5416(1979).
RN   [9]
RP   SEQUENCE OF 110-156 FROM N.A.
RX   MEDLINE=84069777; PubMed=6689067;
RA   Imam A.M., Eaton M.A., Williamson R., Humphries S.;
RT   "Isolation and characterisation of cDNA clones for the A alpha- and
RT   gamma-chains of human fibrinogen.";
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RL   Nucleic Acids Res. 11:7427-7434(1983).
RN   [10]
RP   SEQUENCE OF 605-644 FROM N.A. (ISOFORM ALPHA).
RX   MEDLINE=83254384; PubMed=6575700;
RA   Chung D.W., Rixon M.W., Que B.G., Davie E.W.;
RT   "Cloning of fibrinogen genes and their cDNA.";
RL   Ann. N.Y. Acad. Sci. 408:449-456(1983).
RN   [11]
RP   SEQUENCE OF 20-35.
RA   Blomback B., Blomback M., Grondahl N.J., Guthrie C., Hinton M.;
RT   "Studies on fibrinopeptides from primates.";
RL   Acta Chem. Scand. 19:1788-1789(1965).
RN   [12]
RP   CROSS-LINKING ACCEPTOR SITES.
RX   MEDLINE=80088230; PubMed=518845;
RA   Cottrell B.A., Strong D.D., Watt K.W.K., Doolittle R.F.;
RT   "Amino acid sequence studies on the alpha chain of human fibrinogen.
RT   Exact location of cross-linking acceptor sites.";
RL   Biochemistry 18:5405-5410(1979).
RN   [13]
RP   CROSS-LINKING ACCEPTOR SITES.
RX   MEDLINE=78130085; PubMed=632262;
RA   Fretto L.J., Ferguson E.W., Steinman H.M., McKee P.A.;
RT   "Localization of the alpha-chain cross-link acceptor sites of human
RT   fibrin.";
RL   J. Biol. Chem. 253:2184-2195(1978).
RN   [14]
RP   VARIANT, AND DISULFIDE BONDS.
RX   MEDLINE=76225080; PubMed=936108;
RA   Blombaeck B., Hessel B., Hogg D.;
RT   "Disulfide bridges in NH2-terminal part of human fibrinogen.";
RL   Thromb. Res. 8:639-658(1976).
RN   [15]
RP   REVIEW, EM STRUCTURE, POLYMERIZATION, AND LIGANDS.
RX   MEDLINE=84305751; PubMed=6383194;
RA   Doolittle R.F.;
RT   "Fibrinogen and fibrin.";
RL   Annu. Rev. Biochem. 53:195-229(1984).
RN   [16]
RP   CROSS-LINKING SITE FOR ALPHA-2-PLASMIN INHIBITOR.
RX   MEDLINE=87057190; PubMed=2877981;
RA   Kimura S., Aoki N.;
RT   "Cross-linking site in fibrinogen for alpha 2-plasmin inhibitor.";
RL   J. Biol. Chem. 261:15591-15595(1986).
RN   [17]
RP   PHOSPHORYLATION.
RX   MEDLINE=84104274; PubMed=6318767;
RA   Itarte E., Plana M., Guasch M.D., Martos C.;
RT   "Phosphorylation of fibrinogen by casein kinase 1.";
RL   Biochem. Biophys. Res. Commun. 117:631-636(1983).
RN   [18]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-39.
RX   MEDLINE=92218459; PubMed=1560020;
RA   Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
RT   "The structure of residues 7-16 of the A alpha-chain of human
RT   fibrinogen bound to bovine thrombin at 2.3-A resolution.";
RL   J. Biol. Chem. 267:7911-7920(1992).
RN   [19]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 130-216.
RX   MEDLINE=97472408; PubMed=9333233;
RA   Spraggon G., Everse S.J., Doolittle R.F.;
RT   "Crystal structures of fragment D from human fibrinogen and its
RT   crosslinked counterpart from fibrin.";
RL   Nature 389:455-462(1997).
RN   [20]
RP   X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 130-216.
RX   MEDLINE=98292395; PubMed=9628725;
RA   Everse S.J., Spraggon G., Veerapandian L., Riley M., Doolittle R.F.;
RT   "Crystal structure of fragment double-D from human fibrin with two
RT   different bound ligands.";
RL   Biochemistry 37:8637-8642(1998).
RN   [21]
RP   X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 670-866.
RX   MEDLINE=98356117; PubMed=9689040;
RA   Spraggon G., Applegate D., Everse S.J., Zhang J.Z., Veerapandian L.,
RA   Redman C., Doolittle R.F., Grieninger G.;
RT   "Crystal structure of a recombinant alphaEC domain from human
RT   fibrinogen-420.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:9099-9104(1998).
RN   [22]
RP   X-RAY CRYSTALLOGRAPHY.
RX   MEDLINE=99175089; PubMed=10074346;
RA   Everse S.J., Spraggon G., Veerapandian L., Doolittle R.F.;
RT   "Conformational changes in fragments D and double-D from human
RT   fibrin(ogen) upon binding the peptide ligand Gly-His-Arg-Pro-amide.";
RL   Biochemistry 38:2941-2946(1999).
RN   [23]
RP   VARIANT KYOTO-2.
RX   MEDLINE=91300048; PubMed=2070049;
RA   Yoshida N., Okuma M., Hirata H., Matsuda M., Yamazumi K., Asakura S.;
RT   "Fibrinogen Kyoto II, a new congenitally abnormal molecule,
RT   characterized by the replacement of A alpha proline-18 by leucine.";
RL   Blood 78:149-153(1991).
RN   [24]
RP   VARIANT LIMA.
RX   MEDLINE=92340680; PubMed=1634621;
RA   Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA   Takahashi N., Arocha-Pinango C.L., Rodriguez S., Nagy H.,
RA   Perez-Requejo J.L., Matsuda M.;
RT   "Fibrinogen Lima: a homozygous dysfibrinogen with an A
RT   alpha-arginine-141 to serine substitution associated with extra
RT   N-glycosylation at A alpha-asparagine-139. Impaired fibrin gel
RT   formation but normal fibrin-facilitated plasminogen activation
RT   catalyzed by tissue-type plasminogen activator.";
RL   J. Clin. Invest. 90:67-76(1992).
RN   [25]
RP   VARIANT CARACAS-2.
RX   MEDLINE=91268018; PubMed=1675636;
RA   Maekawa H., Yamazumi K., Muramatsu S., Kaneko M., Hirata H.,
RA   Takahashi N., de Bosch N.B., Carvajal Z., Ojeda A.,
RA   Arocha-Pinango C.L., Matsuda M.;
RT   "An A alpha Ser-434 to N-glycosylated Asn substitution in a
RT   dysfibrinogen, fibrinogen Caracas II, characterized by impaired
RT   fibrin gel formation.";
RL   J. Biol. Chem. 266:11575-11581(1991).
RN   [26]
RP   VARIANT DUSART.
RX   MEDLINE=93232289; PubMed=8473507;
RA   Koopman J., Haverkate F., Grimbergen J., Lord S.T., Mosesson M.W.,
RA   Diorio J.P., Siebenlist K.S., Legrand C., Soria J., Soria C.,
RA   Caen J.P.;
RT   "Molecular basis for fibrinogen Dusart (A alpha 554 Arg-->Cys) and
RT   its association with abnormal fibrin polymerization and
RT   thrombophilia.";

  Query Match             87.7%;  Score 57;  DB 1;  Length 866;
  Best Local Similarity   91.7%;  Pred. No. 0.036;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | ||||||||||
Db         24 EGDFLAEGGGVR 35


RESULT 4
FIBA_CERSI
ID   FIBA_CERSI     STANDARD;      PRT;    16 AA.
AC   P14535;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Ceratotherium simum (White rhinoceros) (Square-lipped rhinoceros).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
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OX   NCBI_TaxID=9807;
RN   [1]
RP   SEQUENCE.
RA   O'Neil P.B., Doolittle R.F.;
RT   "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL   Syst. Zool. 22:590-595(1973).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1639 MW;  0958CBB6293F4C81 CRC64;

  Query Match             86.2%;  Score 56;  DB 1;  Length 16;
  Best Local Similarity   76.9%;  Pred. No. 0.0011;
  Matches   10;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              :| ||:|||||||
Db          4 TEGDFIAEGGGVR 16


RESULT 5
FIBA_TAPTE
ID   FIBA_TAPTE     STANDARD;      PRT;    16 AA.
AC   P14536;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Tapirus terrestris (Lowland tapir) (Brazilian tapir).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX   NCBI_TaxID=9801;
RN   [1]
RP   SEQUENCE.
RA   O'Neil P.B., Doolittle R.F.;
RT   "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL   Syst. Zool. 22:590-595(1973).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1622 MW;  48598EB6292F4030 CRC64;

  Query Match             83.1%;  Score 54;  DB 1;  Length 16;
  Best Local Similarity   76.9%;  Pred. No. 0.0025;
  Matches   10;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              :| :|||||||||
Db          4 TEGEFLAEGGGVR 16


RESULT 6
FIBA_HYLLA
ID   FIBA_HYLLA     STANDARD;      PRT;    16 AA.
AC   P14453;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Hylobates lar (Common gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
OX   NCBI_TaxID=9580;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=70294424; PubMed=5466708;
RA   Mross G.A., Doolittle R.F., Roberts B.F.;
RT   "Gibbon fibrinopeptides: identification of a glycine-serine allelism
RT   at position B-3.";
RL   Science 170:468-470(1970).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1565 MW;  49E98EB63EA04DD3 CRC64;

  Query Match             81.5%;  Score 53;  DB 1;  Length 16;
  Best Local Similarity   83.3%;  Pred. No. 0.0037;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | :||||||||||
Db          5 EGEFLAEGGGVR 16


RESULT 7
FIBA_CAMDR
ID   FIBA_CAMDR     STANDARD;      PRT;    18 AA.
AC   P14444;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Camelus dromedarius (Dromedary) (Arabian camel).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
OX   NCBI_TaxID=9838;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=67209145; PubMed=6033721;
RA   Doolittle R.F., Schubert D., Schwartz S.A.;
RT   "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT   Dromedary camel, mule deer, and cape buffalo.";
RL   Arch. Biochem. Biophys. 118:456-467(1967).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     18       FIBRINOPEPTIDE A.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  1835 MW;  244448763D7F4CC6 CRC64;
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  Query Match             81.5%;  Score 53;  DB 1;  Length 18;
  Best Local Similarity   83.3%;  Pred. No. 0.0042;
  Matches   10;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | :|||||||||
Db          7 EGEFLAEGGGVR 18


RESULT 8
FIBA_BISBO
ID   FIBA_BISBO     STANDARD;      PRT;    19 AA.
AC   P14441;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Bison bonasus (European bison).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bison.
OX   NCBI_TaxID=9902;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     19       FIBRINOPEPTIDE A.
FT   NON_TER      19     19
SQ   SEQUENCE   19 AA;  1836 MW;  9BA55A0F473B59C5 CRC64;

  Query Match             81.5%;  Score 53;  DB 1;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 0.0044;
  Matches   10;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              :  ||||||||||
Db          7 ASGDFLAEGGGVR 19


RESULT 9
FIBA_CERNI
ID   FIBA_CERNI     STANDARD;      PRT;    19 AA.
AC   P14447;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Cervus nippon (Sika deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9863;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J., Holmberg E.;
RT   "Structure of fibrinopeptides-its relation to enzyme specificity and
RT   phylogeny and classification of species.";
RL   Ark. Kemi 25:411-428(1966).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   NON_TER       19     19
SQ   SEQUENCE   19 AA;  1822 MW;  9BA40926873B59C5 CRC64;

  Query Match             81.5%;  Score 53;  DB 1;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 0.0044;
  Matches   10;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              : |:|||||||||
Db          7 ASSEFLAEGGGVR 19


RESULT 10
FIBA_FELCA
ID   FIBA_FELCA     STANDARD;      PRT;    16 AA.
AC   P14450;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1620 MW;  C3C98EB62D6CC7D3 CRC64;

  Query Match             78.5%;  Score 51;  DB 1;  Length 16;
  Best Local Similarity   75.0%;  Pred. No. 0.0084;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | :|:|||||||
Db          5 EGEFIAEGGGVR 16


RESULT 11
FIBA_CANFA
ID   FIBA_CANFA     STANDARD;      PRT;    28 AA.
AC   P02673; P14464;
DT   21-JUL-1986 (Rel. 01, Created)
DT   01-NOV-1990 (Rel. 16, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Canis familiaris (Dog), and
OS   Vulpes vulpes (Red fox).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615, 9627;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=C.familiaris;
RX   MEDLINE=76081726; PubMed=1198547;
RA   Birken S., Wilner G.D., Canfield R.E.;
RT   "Studies of the structure of canine fibrinogen.";
RL   Thromb. Res. 7:599-610(1975).
RN   [2]
RP   SEQUENCE OF 1-16.
RC   SPECIES=C.familiaris, and V.vulpes;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [3]
RP   SEQUENCE OF 1-16.
RC   SPECIES=C.familiaris;
RX   MEDLINE=66020594; PubMed=5836555;
RA   Osbahr A.J. Jr., Colman R.W., Laki K., Gladner J.A.;
RT   "The nature of the peptides released from canine fibrinogen.";
RL   Biochem. Biophys. Res. Commun. 14:555-558(1964).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
DR   PIR; A94308; A05296.
KW   Blood coagulation; Plasma; Phosphorylation.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   MOD_RES       3      3       PHOSPHORYLATION (PARTIAL).
FT   CONFLICT      2      2       N -> D (IN REF. 2).
FT   CONFLICT      4      7       KEGE -> EGKQ (IN REF. 2).
FT   NON_TER      28     28
SQ   SEQUENCE   28 AA;  2958 MW;  09DCD3F923BFEBD2 CRC64;

  Query Match             78.5%;  Score 51;  DB 1;  Length 28;
  Best Local Similarity   75.0%;  Pred. No. 0.014;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | :|:|||||||
Db          5 EGEFIAEGGGVR 16


RESULT 12
FIBA_PIG
ID   FIBA_PIG       STANDARD;      PRT;    17 AA.
AC   P14460;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
DR   PIR; E29501; E29501.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      17     17
SQ   SEQUENCE   17 AA;  1762 MW;  232EFEBB8B6B0A0C CRC64;

  Query Match             75.4%;  Score 49;  DB 1;  Length 17;
  Best Local Similarity   75.0%;  Pred. No. 0.02;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              : :|||||||||
Db          6 KGEFLAEGGGVR 17


RESULT 13
FIBA_LAMGL
ID   FIBA_LAMGL     STANDARD;      PRT;    18 AA.
AC   P14454;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Lama glama (Llama), and
OS   Lama vicugna (Vicugna) (Vicugna vicugna).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
OX   NCBI_TaxID=9844, 9843;
RN   [1]
RP   SEQUENCE.
RC   SPECIES=L.glama;
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
RN   [2]
RP   SEQUENCE.
RC   SPECIES=L.vicugna;
RA   Mross G.A., Doolittle R.F.;
RT   "Amino acid sequence studies on artiodacty fibrinopeptides.";
RL   Arch. Biochem. Biophys. 122:674-684(1967).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     18       FIBRINOPEPTIDE A.
FT   NON_TER      18     18
SQ   SEQUENCE   18 AA;  1834 MW;  2444487B8B7F4CC6 CRC64;

  Query Match             75.4%;  Score 49;  DB 1;  Length 18;
  Best Local Similarity   75.0%;  Pred. No. 0.021;
  Matches    9;  Conservative    2;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              : :|||||||||
Db          7 KGEFLAEGGGVR 18


RESULT 14
FIBA_SYNCA
ID   FIBA_SYNCA     STANDARD;      PRT;    15 AA.
AC   P14463;
DT   01-JAN-1990 (Rel. 13, Created)
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```
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Syncerus caffer (Cape buffalo).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Syncerus.
OX   NCBI_TaxID=9970;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=67209145; PubMed=6033721;
RA   Doolittle R.F., Schubert D., Schwartz S.A.;
RT   "Amino acid sequence studies on artiodactyl fibrinopeptides. I.
RT   Dromedary camel, mule deer, and cape buffalo.";
RL   Arch. Biochem. Biophys. 118:456-467(1967).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     15       FIBRINOPEPTIDE A.
FT   NON_TER      15     15
SQ   SEQUENCE   15 AA;  1480 MW;  4E998EA5F0B41CC6 CRC64;

  Query Match             73.8%;  Score 48;  DB 1;  Length 15;
  Best Local Similarity   90.0%;  Pred. No. 0.026;
  Matches    9;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DFLAEGGGVR 13
              :||||||||||
Db          6 EFLAEGGGVR 15


RESULT 15
FIBA_EQUAS
ID   FIBA_EQUAS     STANDARD;      PRT;    16 AA.
AC   P14449;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN   FGA.
OS   Equus asinus (Donkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9793;
RN   [1]
RP   SEQUENCE.
RA   Blomback B., Blomback M., Grondahl N.J.;
RT   "Studies on fibrinopeptides from mammals.";
RL   Acta Chem. Scand. 19:1789-1791(1965).
CC   -!- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC       polymerize into fibrin and acting as a cofactor in platelet
CC       aggregation.
CC   -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
CC       (ALPHA, BETA AND GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
CC   -!- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC       which cleaves fibrinopeptides A and B from alpha and beta chains,
CC       and thus exposes the N-terminal polymerization sites responsible
CC       for the formation of the soft clot.
KW   Blood coagulation; Plasma.
FT   PEPTIDE       1     16       FIBRINOPEPTIDE A.
FT   NON_TER      16     16
SQ   SEQUENCE   16 AA;  1696 MW;  09598EB63C2A5957 CRC64;

  Query Match             73.8%;  Score 48;  DB 1;  Length 16;
  Best Local Similarity   66.7%;  Pred. No. 0.028;
  Matches    8;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              | :|::||||||
Db          5 EGEFISEGGGVR 16


Search completed: April 27, 2004, 16:24:21
Job time : 11 secs
```

OM protein - protein search, using sw model

Run on: April 27, 2004, 16:22:48 ; Search time 39 Seconds
(without alignments)
105.173 Million cell updates/sec

Title: US-09-845-729A-1_COPY_2_14
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	57	87.7	218	4	Q8WW76	Q8ww76 homo sapien
2	46	70.8	557	11	Q99K47	Q99k47 mus musculu
3	43	66.2	260	10	Q8S2N9	Q8s2n9 oryza sativ
4	41	63.1	242	5	Q8T925	Q8t925 tetrahymena
5	41	63.1	552	2	Q9APX1	Q9apx1 pseudomonas
6	40	61.5	280	16	Q99WM6	Q99wm6 staphylococ
7	40	61.5	280	16	Q8NY96	Q8ny96 staphylococ
8	40	61.5	401	10	Q850S5	Q850s5 oryza sativ
9	40	61.5	630	13	Q8UW15	Q8uw15 lapemis har
10	40	61.5	852	5	Q9U4G5	Q9u4g5 drosophila
11	39	60.0	89	16	Q98F73	Q98f73 rhizobium l
12	39	60.0	171	3	Q9P8L5	Q9p8l5 botrytis ci
13	39	60.0	186	2	Q9F7D5	Q9f7d5 salmonella
14	39	60.0	245	16	Q9Z4S4	Q9z4s4 salmonella
15	39	60.0	245	16	Q8Z6K4	Q8z6k4 salmonella
16	39	60.0	324	16	O53481	O53481 mycobacteri
17	39	60.0	324	16	Q7TZ37	Q7tz37 mycobacteri
18	39	60.0	365	16	Q823I9	Q823i9 chlamydophi
19	39	60.0	450	16	Q8P973	Q8p973 xanthomonas
20	39	60.0	462	10	Q8LFX3	Q8lfx3 arabidopsis
21	39	60.0	465	10	Q9LH81	Q9lh81 arabidopsis
22	39	60.0	465	10	Q940V4	Q940v4 arabidopsis
23	39	60.0	481	10	Q8W0R4	Q8w0r4 sorghum bic
24	39	60.0	546	5	Q9VHD0	Q9vhd0 drosophila
25	39	60.0	580	10	Q7XN79	Q7xn79 oryza sativ
26	39	60.0	705	2	O85866	O85866 sphingomona
27	39	60.0	748	10	Q8W0N1	Q8w0n1 oryza sativ
28	39	60.0	753	10	Q9LIC9	Q9lic9 arabidopsis
29	39	60.0	753	10	Q8L741	Q8l741 arabidopsis
30	39	60.0	1159	4	Q9NY34	Q9ny34 homo sapien
31	39	60.0	1165	4	Q9NZQ8	Q9nzq8 homo sapien
32	38.5	59.2	741	16	Q8UFY1	Q8ufy1 agrobacteri
33	38	58.5	77	10	Q84SA5	Q84sa5 aster tripo
34	38	58.5	99	16	Q8ZQ92	Q8zq92 salmonella
35	38	58.5	147	10	Q9MAV0	Q9mav0 arabidopsis
36	38	58.5	155	16	Q8ELS7	Q8els7 oceanobacil
37	38	58.5	195	16	Q8EAT0	Q8eat0 shewanella
38	38	58.5	256	16	Q92LM7	Q92lm7 rhizobium m
39	38	58.5	548	2	Q845J1	Q845j1 pseudomonas
40	38	58.5	575	10	Q8H147	Q8h147 arabidopsis
41	38	58.5	575	10	Q9LZM8	Q9lzm8 arabidopsis
42	38	58.5	575	10	Q8LGJ2	Q8lgj2 arabidopsis
43	38	58.5	611	4	Q8WYK5	Q8wyk5 homo sapien
44	38	58.5	611	11	Q8BGD9	Q8bgd9 mus musculu
45	38	58.5	652	16	Q8YPV7	Q8ypv7 anabaena sp

ALIGNMENTS

RESULT 1
Q8WW76
ID Q8WW76 PRELIMINARY; PRT; 218 AA.
AC Q8WW76;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Similar to fibrinogen, A alpha polypeptide.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC020764; AAH20764.1; -.
SQ SEQUENCE 218 AA; 24695 MW; 36D756A8116EA94A CRC64;

Query Match 87.7%; Score 57; DB 4; Length 218;
Best Local Similarity 91.7%; Pred. No. 0.045;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 ESDFLAEGGGVR 13
              | ||||||||||
Db         24 EGDFLAEGGGVR 35
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RESULT 2
Q99K47
ID Q99K47 PRELIMINARY; PRT; 557 AA.
AC Q99K47;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Fibrinogen A alpha polypeptide.
GN FGA.
OS Mus musculus (Mouse).

```
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Strausberg R.;
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC005467; AAH05467.1; -.
DR   HSSP; P02671; 1FZA.
DR   MGD; MGI:1316726; Fga.
SQ   SEQUENCE   557 AA;  61325 MW;  C47F496D1BA432DE CRC64;

  Query Match             70.8%;  Score 46;  DB 11;  Length 557;
  Best Local Similarity   66.7%;  Pred. No. 12;
  Matches    8;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 ESDFLAEGGGVR 13
              : :||:||||||
Db         25 KGEFLSEGGGVR 36


RESULT 3
Q8S2N9
ID   Q8S2N9      PRELIMINARY;      PRT;   260 AA.
AC   Q8S2N9;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   B1066G12.16 protein (B1008C01.2 protein).
GN   B1066G12.16 OR B1008C01.2.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT   clone:B1066G12.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
RT   clone:B1008C01.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP003201; BAB89442.1; -.
DR   EMBL; AP003196; BAB93122.1; -.
DR   Gramene; Q8S2N9; -.
SQ   SEQUENCE   260 AA;  29524 MW;  40929C6C486F0F06 CRC64;

  Query Match             66.2%;  Score 43;  DB 10;  Length 260;
  Best Local Similarity   69.2%;  Pred. No. 18;
  Matches    9;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              |||| :||| |:|
Db        188 SESDPVAEGSGLR 200


RESULT 4
Q8T925
ID   Q8T925      PRELIMINARY;      PRT;   242 AA.
AC   Q8T925;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Igr2p.
GN   IGR2.
OS   Tetrahymena thermophila.
OC   Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC   Tetrahymenina; Tetrahymena.
OX   NCBI_TaxID=5911;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Turkewitz A.P., Haddad A.;
RT   "A non-architectural cargo protein in Tetrahymena thermophila dense
RT   core secretory granules.";
RL   Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: CONTAINS 1 C2 DOMAIN.
DR   EMBL; AY075152; AAL79515.1; -.
DR   InterPro; IPR000008; C2.
DR   InterPro; IPR008973; C2_CaLB.
DR   InterPro; IPR006031; XYPPX.
DR   Pfam; PF00168; C2; 1.
DR   Pfam; PF02162; XYPPX; 9.
DR   SMART; SM00239; C2; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
SQ   SEQUENCE   242 AA;  27000 MW;  A1E687237B618E8A CRC64;

  Query Match             63.1%;  Score 41;  DB 5;  Length 242;
  Best Local Similarity   70.0%;  Pred. No. 38;
  Matches    7;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGG 10
              |::||:||||
Db         77 SKNDFIAEGG 86


RESULT 5
Q9APX1
ID   Q9APX1      PRELIMINARY;      PRT;   552 AA.
AC   Q9APX1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Putative amino acid transport protein.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21142509; PubMed=11208781;
RA   Liang X., Pham X.Q.T., Olson M.V., Lory S.;
RT   "Identification of a Genomic Island Present in the Majority of
RT   Pathogenic Isolates of Pseudomonas aeruginosa.";
RL   J. Bacteriol. 183:843-853(2001).
DR   EMBL; AF241171; AAK01502.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR001734; Na/solut_symport.
DR   Pfam; PF00474; SSF; 1.
DR   TIGRFAMs; TIGR00813; sss; 1.
DR   PROSITE; PS00456; NA_SOLUT_SYMP_1; 1.
DR   PROSITE; PS50283; NA_SOLUT_SYMP_3; 1.
SQ   SEQUENCE   552 AA;  58956 MW;  7A45F15BC8865C09 CRC64;

  Query Match             63.1%;  Score 41;  DB 2;  Length 552;
  Best Local Similarity   53.8%;  Pred. No. 93;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              | :|| : |||:|
Db         58 STADFYSAGGGIR 70


RESULT 6
Q99WM6
ID   Q99WM6      PRELIMINARY;      PRT;   280 AA.
AC   Q99WM6;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
```

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DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein SAV0351.
GN   SAV0351 OR SA0339.
OS   Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS   Staphylococcus aureus (strain N315).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=158878, 158879;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX   MEDLINE=21311952; PubMed=11418146;
RA   Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA   Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA   Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA   Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA   Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA   Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA   Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT   "Whole genome sequencing of meticillin-resistant Staphylococcus
RT   aureus.";
RL   Lancet 357:1225-1240(2001).
DR   EMBL; AP003359; BAB56513.1; -.
DR   EMBL; AP003130; BAB41563.1; -.
DR   PIR; H89800; H89800.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   SMART; SM00382; AAA; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   280 AA;  31464 MW;  2B0B9CF79F341652 CRC64;

  Query Match            61.5%;  Score 40;  DB 16;  Length 280;
  Best Local Similarity  66.7%;  Pred. No. 67;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DFLAEGGGV 12
              ||:|:|||:
Db        176 DFVAQGGGI 184


RESULT 7
Q8NY96
ID   Q8NY96      PRELIMINARY;      PRT;   280 AA.
AC   Q8NY96;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   MW0327 protein.
GN   MW0327.
OS   Staphylococcus aureus (strain MW2).
OC   Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX   NCBI_TaxID=196620;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22040717; PubMed=12044378;
RA   Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA   Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA   Yamamoto K., Hiramatsu K.;
RT   "Genome and virulence determinants of high virulence community-
RT   acquired MRSA.";
RL   Lancet 359:1819-1827(2002).
DR   EMBL; AP004823; BAB94192.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00005; ABC_tran; 1.
DR   ProDom; PD000006; ABC_transporter; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
KW   Complete proteome.
SQ   SEQUENCE   280 AA;  31511 MW;  5AD98FDB4DF192B8 CRC64;

  Query Match            61.5%;  Score 40;  DB 16;  Length 280;
  Best Local Similarity  66.7%;  Pred. No. 67;
  Matches    6;  Conservative    3;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 DFLAEGGGV 12
              ||:|:|||:
Db        176 DFVAQGGGI 184


RESULT 8
Q850S5
ID   Q850S5      PRELIMINARY;      PRT;   401 AA.
AC   Q850S5;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Putative hydroxylase.
GN   OSJNBB0047K21.13.
OS   Oryza sativa (japonica cultivar-group).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=39947;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. Nipponbare;
RA   Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Jenkins C.N., Hsiao J.,
RA   Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E., Craven B.,
RA   Khalak H., Feldblyum T.V., Quackenbush J., White O., Salzberg S.L.,
RA   Fraser C.M.;
RT   "Oryza sativa chromosome 3 BAC OSJNBb0047K21 genomic sequence.";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC135600; AAO23096.1; -.
DR   GO; GO:0006118; P:electron transport; IEA.
DR   InterPro; IPR001128; Cytochrome_P450.
DR   Pfam; PF00067; p450; 1.
DR   PRINTS; PR00385; P450.
DR   PROSITE; PS00086; CYTOCHROME_P450; 1.
SQ   SEQUENCE   401 AA;  45588 MW;  3F9218635A57FF4F CRC64;

  Query Match            61.5%;  Score 40;  DB 10;  Length 401;
  Best Local Similarity  53.8%;  Pred. No. 99;
  Matches    7;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              :  ||:| |||:|
Db        336 ASKDFMAFGGGLR 348


RESULT 9
Q8UW15
ID   Q8UW15      PRELIMINARY;      PRT;   630 AA.
AC   Q8UW15;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Eukaryotic translation inititation factor 4B.
GN   EIF4B.
OS   Lapemis hardwickii (Hardwick's sea snake).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC   Elapidae; Hydrophiinae; Lapemis.
OX   NCBI_TaxID=8781;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RA   Xu A., Wei J., Yang W., Zhao G., Zhong X.;
RT   "A novel eukaryotic translation initiation factor 4B cDNA clone from
RT   sea snake.";
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF165225; AAL54908.1; -.
DR   GO; GO:0003676; F:nucleic acid binding; IEA.
DR   InterPro; IPR000504; RNA_rec_mot.
DR   Pfam; PF00076; rrm; 1.
DR   SMART; SM00360; RRM; 1.
DR   PROSITE; PS50102; RRM; 1.
DR   PROSITE; PS00030; RRM_RNP_1; 1.
SQ   SEQUENCE   630 AA;  71186 MW;  E3457B6ED3502A16 CRC64;

  Query Match             61.5%;  Score 40;  DB 13;  Length 630;
  Best Local Similarity   88.9%;  Pred. No. 1.6e+02;
  Matches    8;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 SDFLAEGGG 11
              |||||| ||
Db         18 SDFLAEDGG 26


RESULT 10
Q9U4G5
ID   Q9U4G5      PRELIMINARY;      PRT;   852 AA.
AC   Q9U4G5; Q9VQB2;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   BCDNA:GH09817 protein.
GN   BCDNA:GH09817 OR CG4272.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC   Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Berkeley;
RA   Rubin G.M., Wan K.H., Harvey D., Lewis S.E., Brokstein P., Tsang G.,
RA   Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C.,
RA   Champe M., Chavez C., Chew M., Doyle C.M., Farfan D.E., Frise E.,
RA   Galle R., George R.A., Harris N.L., Hoskins R.A., Evans-Holm M.,
RA   Houston K.A., Hummasti S.R., Kim E., Li P., Moshrefi M., Pacleb J.M.,
RA   Park S., Sequeira A., Sethi H., Snir E., Svirskas R.R., Weinburg T.,
RA   Celniker S.E.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE003583; AAF51264.1; ALT_INIT.
DR   EMBL; AF181640; AAD55426.1; -.
DR   FlyBase; FBgn0028485; BcDNA:GH09817.
KW   Hypothetical protein.
SQ   SEQUENCE   852 AA;  91073 MW;  B87C3607203DA4EC CRC64;

  Query Match             61.5%;  Score 40;  DB 5;  Length 852;
  Best Local Similarity   63.6%;  Pred. No. 2.3e+02;
  Matches    7;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGG 11
              || |:|:|| |
Db        376 SEEDYLSEGSG 386


RESULT 11
Q98F73
ID   Q98F73      PRELIMINARY;      PRT;    89 AA.
AC   Q98F73;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Hypothetical protein msl3900.
GN   MSL3900.
OS   Rhizobium loti (Mesorhizobium loti).
OC   Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC   Phyllobacteriaceae; Mesorhizobium.
OX   NCBI_TaxID=381;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MAFF303099;
RX   MEDLINE=21082930; PubMed=11214968;
RA   Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA   Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA   Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA   Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT   Mesorhizobium loti.";
RL   DNA Res. 7:331-338(2000).
DR   EMBL; AP003003; BAB50694.1; -.
DR   InterPro; IPR006339; AbrB_trans_reg.
DR   InterPro; IPR007159; SpoVT_AbrB.
DR   Pfam; PF04014; SpoVT_AbrB; 1.
DR   TIGRFAMs; TIGR01439; lp_hng_hel_AbrB; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   89 AA;  10058 MW;  5197B7CB06AFC351 CRC64;

  Query Match             60.0%;  Score 39;  DB 16;  Length 89;
  Best Local Similarity   61.5%;  Pred. No. 29;
  Matches    8;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              || :|:|  ||||
Db         25 SEVEFVATDGGVR 37
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RESULT 12
Q9P8L5
ID   Q9P8L5      PRELIMINARY;      PRT;   171 AA.
AC   Q9P8L5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   ABC transporter-like protein (Fragment).
GN   BCATRJ.
OS   Botrytis cinerea (Noble rot fungus) (Botryotinia fuckeliana).
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes;
OC   Helotiales; Sclerotiniaceae; Botryotinia.
OX   NCBI_TaxID=40559;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=B05.10;
RA   Schoonbeek H., Vermeulen T., Hayashi K., De Waard M.A.;
RT   "Differential expression of membrane-bound transporters in Botrytis
RT   cinerea.";
RL   Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF238228; AAF64438.1; -.
DR   InterPro; IPR004147; ABC1.
DR   Pfam; PF03109; ABC1; 1.
FT   NON_TER       1      1
FT   NON_TER     171    171
SQ   SEQUENCE   171 AA;  19561 MW;  15515C19C9FBB1F9 CRC64;

  Query Match             60.0%;  Score 39;  DB 3;  Length 171;
  Best Local Similarity   70.0%;  Pred. No. 59;
  Matches    7;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 SDFLAEGGGV 12
              |||:  ||||
Db        159 SDFMENGGGV 168


RESULT 13
Q9F7D5
ID   Q9F7D5      PRELIMINARY;      PRT;   186 AA.
AC   Q9F7D5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein (Fragment).
GN   NTT.
OS   Salmonella enterica subsp. enterica serovar Typhimurium.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=90371;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RX   MEDLINE=21172862; PubMed=11274105;
RA   Price-Carter M., Tingey J., Bobik T.A., Roth J.R.;
RT   "The Alternative Electron Acceptor Tetrathionate Supports B12-
RT   Dependent Anaerobic Growth of Salmonella enterica Serovar Typhimurium
RT   on Ethanolamine or 1,2-Propanediol.";
RL   J. Bacteriol. 183:2463-2475(2001).
DR   EMBL; AF282268; AAG31761.1; -.
KW   Hypothetical protein.
FT   NON_TER     186    186
SQ   SEQUENCE   186 AA;  20711 MW;  6B5FE0B04E07CFA0 CRC64;

  Query Match             60.0%;  Score 39;  DB 2;  Length 186;
  Best Local Similarity   60.0%;  Pred. No. 65;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SDFLAEGGGV 12
              :|::|||||:
Db        102 ADYVAEGGGL 111


RESULT 14
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Q9Z4S4
ID   Q9Z4S4      PRELIMINARY;      PRT;   245 AA.
AC   Q9Z4S4;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE   ORF 245 protein (Putative cytoplasmic protein).
GN   ORF245 OR STM1381.
OS   Salmonella typhimurium.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RX   MEDLINE=99157556; PubMed=10027966;
RA   Hensel M., Egelseer C., Nikolaus T.;
RT   "Molecular and functional analysis indicates a mosaic structure of
RT   Salmonella Pathogenicity Island 2.";
RL   Mol. Microbiol. 31:489-498(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2;
RA   Hensel M., Hinsley A.P., Nikolaus T., Sawers G., Berks B.C.;
RT   "he genetic basis of tetrathionate respiration in Salmonella
RT   typhimurium.";
RL   Mol. Microbiol. 0:0-0(0).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
DR   EMBL; AJ224978; CAB37418.1; -.
DR   EMBL; AE008760; AAL20305.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   245 AA;  27430 MW;  FFBF31AA9DC8E943 CRC64;

  Query Match             60.0%;  Score 39;  DB 16;  Length 245;
  Best Local Similarity   60.0%;  Pred. No. 88;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SDFLAEGGGV 12
              :|::|||||:
Db        102 ADYVAEGGGL 111


RESULT 15
Q8Z6K4
ID   Q8Z6K4      PRELIMINARY;      PRT;   245 AA.
AC   Q8Z6K4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Orf 245 protein.
GN   STY1741 OR T1249.
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
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RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Ty2 / ATCC 700931;
RX   MEDLINE=22531367; PubMed=12644504;
RA   Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA   Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT   "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT   and CT18.";
RL   J. Bacteriol. 185:2330-2337(2003).
DR   EMBL; AL627271; CAD01984.1; -.
DR   EMBL; AE016838; AAO68902.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   PROSITE; PS00290; IG_MHC; 1.
KW   Complete proteome.
SQ   SEQUENCE   245 AA;  27429 MW;  11BF3BA03D62E3E3 CRC64;

  Query Match             60.0%;  Score 39;  DB 16;  Length 245;
  Best Local Similarity   60.0%;  Pred. No. 88;
  Matches    6;  Conservative    4;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 SDFLAEGGGV 12
              :|::|||||:
Db        102 ADYVAEGGGL 111


Search completed: April 27, 2004, 16:25:47
Job time : 39 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: April 27, 2004, 16:22:47 ; Search time 55 Seconds
(without alignments)
66.784 Million cell updates/sec

Title: US-09-845-729A-1_COPY_2_14
Perfect score: 65
Sequence: 1 SESDFLAEGGGVR 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65	100.0	13	6	ABG76139	Abg76139 Human alp
2	65	100.0	15	6	ABU08830	Abu08830 Alpha fib
3	65	100.0	15	6	ABG76138	Abg76138 Human alp
4	57	87.7	12	6	ABU09252	Abu09252 Human alp
5	57	87.7	13	6	ABU08825	Abu08825 Alpha fib
6	57	87.7	13	6	ADA18539	Ada18539 Human alp
7	57	87.7	14	6	ABU08827	Abu08827 Alpha fib
8	57	87.7	16	2	AAR96194	Aar96194 Fibrinoge
9	57	87.7	16	2	AAW04619	Aaw04619 Fibrinope
10	57	87.7	16	2	AAY57487	Aay57487 Antimicro
11	57	87.7	16	4	ABB56219	Abb56219 Vascular
12	57	87.7	16	4	AAB91959	Aab91959 Fibronect
13	57	87.7	16	4	ABB52337	Abb52337 Human API
14	57	87.7	16	5	ABG73668	Abg73668 Linear HI
15	57	87.7	16	5	ABG78799	Abg78799 Multiple
16	57	87.7	16	5	ABG70000	Abg70000 Antimicro
17	57	87.7	16	5	ABG69911	Abg69911 Rabbit pl
18	57	87.7	16	6	ABP60019	Abp60019 Biopolyme
19	57	87.7	16	6	ABP60640	Abp60640 Fibrinope
20	57	87.7	16	6	ADA18542	Ada18542 Human alp
21	57	87.7	16	6	ABR58740	Abr58740 Alzheimer
22	57	87.7	17	2	AAR96184	Aar96184 Fibrinoge
23	57	87.7	17	4	AAB91960	Aab91960 Fibronect
24	57	87.7	17	6	ABU08833	Abu08833 Alpha fib
25	57	87.7	17	6	ABU09101	Abu09101 Alpha fib
26	57	87.7	17	6	AAE34820	Aae34820 Staphyloc
27	57	87.7	18	2	AAR96193	Aar96193 Fibrinoge
28	57	87.7	18	6	ABU08834	Abu08834 Alpha fib
29	57	87.7	18	6	ABU08837	Abu08837 Alpha fib
30	57	87.7	18	6	ADA18541	Ada18541 Human alp
31	57	87.7	19	2	AAR96192	Aar96192 Fibrinoge
32	57	87.7	20	2	AAR96191	Aar96191 Fibrinoge
33	57	87.7	20	2	AAY57488	Aay57488 Antimicro
34	57	87.7	20	5	ABG69912	Abg69912 Rabbit pl
35	57	87.7	20	6	AAO27086	Aao27086 Fibrinoge
36	57	87.7	20	6	AAO27084	Aao27084 Fibrinoge
37	57	87.7	20	6	AAO27085	Aao27085 Fibrinoge
38	57	87.7	20	6	AAO27081	Aao27081 Fibrinoge
39	57	87.7	21	2	AAR96183	Aar96183 Fibrinoge
40	57	87.7	22	1	AAP90276	Aap90276 Antigen p
41	57	87.7	22	2	AAR96190	Aar96190 Fibrinoge
42	57	87.7	22	2	AAR96182	Aar96182 Fibrinoge
43	57	87.7	24	5	AAO21114	Aao21114 Anti-angi
44	57	87.7	24	5	AAO21113	Aao21113 Anti-angi
45	57	87.7	24	5	AAO21118	Aao21118 Anti-angi

ALIGNMENTS

RESULT 1
ABG76139
ID ABG76139 standard; peptide; 13 AA.
XX
AC ABG76139;
XX
DT 08-MAY-2003 (first entry)
XX
DE Human alpha fibrinogen peptide #2.
XX
KW Human; alpha fibrinogen; renal failure; myocardial infarction;
KW unstable angina; matrix assisted laser desorption-time of flight;
KW MALDI-TOF; mass spectroscopy; antigen.
XX
OS Homo sapiens.
XX
PN US2002160528-A1.
XX
PD 31-OCT-2002.
XX
PF 30-APR-2001; 2001US-00845729.
XX
PR 30-APR-2001; 2001US-00845729.
XX
PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX
PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
DR WPI; 2003-255194/25.
XX
PT Novel biopolymer marker such as alpha fibrinogen having specific
PT molecular weight, useful in indicating disease state such as myocardial
PT infarction or renal failure.
XX
PS Claim 1; Page 7; 10pp; English.
XX
CC The invention relates a biopolymer marker such as alpha fibrinogen having
CC a molecular weight of about 1350 daltons and a sequence appearing as
CC ABG76139 useful in indicating at least one particular disease state. The
CC presence of the peptide in a sample is determined by matrix assisted
CC laser desorption-time of flight (MALDI-TOF) mass spectroscopy. The marker
CC is useful for indicating at least one particular disease state such as
CC myocardial infarction or renal failure (e.g. in a patient presenting with
CC unstable angina). The biopolymer marker is useful as antigen in

```
CC   immunoassays for the detection of those individuals suffering from the
CC   disease known to be evidenced by the marker sequence. The biopolymer
CC   marker rapidly and accurately diagnoses a disease state such as
CC   myocardial infarction or renal failure, and allows physicians to identify
CC   asymptomatic patients before they suffer from the disease state. The
CC   present sequence is an alpha fibrinogen biopolymer marker
XX
SQ   Sequence 13 AA;

  Query Match            100.0%;  Score 65;  DB 6;  Length 13;
  Best Local Similarity  100.0%;  Pred. No. 0.00024;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              |||||||||||||
Db          1 SESDFLAEGGGVR 13


RESULT 2
ABU08830
ID   ABU08830 standard; peptide; 15 AA.
XX
AC   ABU08830;
XX
DT   25-AUG-2003  (first entry)
XX
DE   Alpha fibrinogen peptide, #4, for physiological condition diagnostics.
XX
KW   Proteomic; human; physiological condition; analyte; biopolymer;
KW   biomarker; alpha fibrinogen; renal failure; myocardial infarction; MI.
XX
OS   Homo sapiens.
XX
PN   US2002160420-A1.
XX
PD   31-OCT-2002.
XX
PF   30-APR-2001; 2001US-00846330.
XX
PR   30-APR-2001; 2001US-00846330.
XX
PA   (JACK/) JACKOWSKI G.
PA   (THAT/) THATCHER B.
PA   (MARS/) MARSHALL J.
PA   (YANT/) YANTHA J.
PA   (VREE/) VREES T.
XX
PI   Jackowski G,  Thatcher B,  Marshall J,  Yantha J,  Vrees T;
XX
DR   WPI; 2003-491923/46.
XX
PT   Determining proteomic basis e.g. basis for diagnosing existence of or
PT   predicting development and/or progression of abnormal physiological
PT   conditions based upon the presence of proteomic materials.
XX
PS   Disclosure; Page 12; 25pp; English.
XX
CC   The invention discloses a method for determining a proteomic basis for
CC   development and progression of abnormal physiological conditions. The
CC   method comprises isolating one or more patient specific proteomic
CC   materials from a sample and comparing it against a library of proteomic
CC   materials having characteristics identifiable with both normal and
CC   abnormal physiological conditions or their predictive hallmarks. The
CC   method is useful for determining a proteomic basis for development and
CC   progression of abnormal physiological conditions. The method is also
CC   useful for evaluating samples containing several analytes/biopolymers for
CC   the presence of physiological condition specific sequences. The peptide
CC   presented is a biomarker from alpha fibrinogen and is associated with
CC   myocardial infarction (MI) and renal failure
XX
SQ   Sequence 15 AA;

  Query Match            100.0%;  Score 65;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 0.00028;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              |||||||||||||
Db          2 SESDFLAEGGGVR 14


RESULT 3
ABG76138
ID   ABG76138 standard; peptide; 15 AA.
XX
AC   ABG76138;
XX
DT   08-MAY-2003  (first entry)
XX
DE   Human alpha fibrinogen peptide #1.
XX
KW   Human; alpha fibrinogen; renal failure; myocardial infarction;
KW   unstable angina; matrix assisted laser desorption-time of flight;
KW   MALDI-TOF; mass spectroscopy; antigen.
XX
OS   Homo sapiens.
XX
PN   US2002160528-A1.
XX
PD   31-OCT-2002.
XX
PF   30-APR-2001; 2001US-00845729.
XX
PR   30-APR-2001; 2001US-00845729.
XX
PA   (JACK/) JACKOWSKI G.
PA   (THAT/) THATCHER B.
PA   (MARS/) MARSHALL J.
PA   (YANT/) YANTHA J.
PA   (VREE/) VREES T.
XX
PI   Jackowski G,  Thatcher B,  Marshall J,  Yantha J,  Vrees T;
XX
DR   WPI; 2003-255194/25.
XX
PT   Novel biopolymer marker such as alpha fibrinogen having specific
PT   molecular weight, useful in indicating disease state such as myocardial
PT   infarction or renal failure.
XX
PS   Disclosure; Fig 1; 10pp; English.
XX
CC   The invention relates a biopolymer marker such as alpha fibrinogen having
CC   a molecular weight of about 1350 daltons and a sequence appearing as
CC   ABG76139 useful in indicating at least one particular disease state. The
CC   presence of the peptide in a sample is determined by matrix assisted
CC   laser desorption-time of flight (MALDI-TOF) mass spectroscopy. The marker
CC   is useful for indicating at least one particular disease state such as
CC   myocardial infarction or renal failure (e.g. in a patient presenting with
CC   unstable angina). The biopolymer marker is useful as antigen in
CC   immunoassays for the detection of those individuals suffering from the
CC   disease known to be evidenced by the marker sequence. The biopolymer
CC   marker rapidly and accurately diagnoses a disease state such as
CC   myocardial infarction or renal failure, and allows physicians to identify
CC   asymptomatic patients before they suffer from the disease state. The
CC   present sequence is an alpha fibrinogen biopolymer marker
XX
SQ   Sequence 15 AA;

  Query Match            100.0%;  Score 65;  DB 6;  Length 15;
  Best Local Similarity  100.0%;  Pred. No. 0.00028;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 SESDFLAEGGGVR 13
              |||||||||||||
Db          2 SESDFLAEGGGVR 14
```

RESULT 4
ABU09252
ID ABU09252 standard; peptide; 12 AA.
XX
AC ABU09252;
XX
DT 24-JUN-2003 (first entry)
XX
DE Human alpha fibrinogen peptide.
XX
KW Human; alpha fibrinogen; renal failure; Syndrome X; insulin resistance;
KW dyslipidaemia; hypertension; obesity; non-insulin dependent diabetes.
XX
OS Homo sapiens.
XX
PN US2002161185-A1.
XX
PD 31-OCT-2002.
XX
PF 30-APR-2001; 2001US-00845725.
XX
PR 30-APR-2001; 2001US-00845725.
XX
PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX
PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
DR WPI; 2003-370707/35.
XX
PT Novel biopolymer marker useful for indicating a particular disease state,
PT e.g. renal failure, comprises a peptide sequence of 12 amino-acids.
XX
PS Claim 1; Page 7; 10pp; English.
XX
CC The invention relates to a biopolymer marker useful for indicating at
CC least one particular disease state e.g. renal failure. The biopolymer
CC marker is useful for developing diagnostic test to identify asymptomatic
CC patients before they suffer an irreversible event. The biopolymer marker
CC enables a diagnostician to gain the ability to characterise either the
CC presence or absence of the at least one disease state relative to the
CC recognition of the presence or absence of the biopolymer. The marker may
CC be of particular use in early diagnosis of Syndrome X, a multi-faceted
CC disease characterised by insulin resistance, dyslipidaemia, hypertension,
CC obesity and non-insulin dependent diabetes. The present sequence is the
CC biopolymer marker of the invention being a peptide derived from human
CC alpha fibrinogen
XX
SQ Sequence 12 AA;

Query Match 87.7%; Score 57; DB 6; Length 12;
Best Local Similarity 91.7%; Pred. No. 0.0051;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
|||||||||||
Db 1 EGDFLAEGGGVR 12

RESULT 5
ABU08825
ID ABU08825 standard; peptide; 13 AA.
XX
AC ABU08825;
XX
DT 25-AUG-2003 (first entry)
XX
DE Alpha fibrinogen peptide, #2, used for myocardial infarction diagnostics.
XX
KW Proteomic; human; physiological condition; analyte; biopolymer;
KW biomarker; alpha fibrinogen; myocardial infarction; MI.
XX
OS Homo sapiens.
XX
PN US2002160420-A1.
XX
PD 31-OCT-2002.
XX
PF 30-APR-2001; 2001US-00846330.
XX
PR 30-APR-2001; 2001US-00846330.
XX
PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX
PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
DR WPI; 2003-491923/46.
XX
PT Determining proteomic basis e.g. basis for diagnosing existence of or
PT predicting development and/or progression of abnormal physiological
PT conditions based upon the presence of proteomic materials.
XX
PS Disclosure; Page 10; 25pp; English.
XX
CC The invention discloses a method for determining a proteomic basis for
CC development and progression of abnormal physiological conditions. The
CC method comprises isolating one or more patient specific proteomic
CC materials from a sample and comparing it against a library of proteomic
CC materials having characteristics identifiable with both normal and
CC abnormal physiological conditions or their predictive hallmarks. The
CC method is useful for determining a proteomic basis for development and
CC progression of abnormal physiological conditions. The method is also
CC useful for evaluating samples containing several analytes/biopolymers for
CC the presence of physiological condition specific sequences. The peptide
CC presented is a biomarker from alpha fibrinogen and is associated with
CC myocardial infarction (MI)
XX
SQ Sequence 13 AA;

Query Match 87.7%; Score 57; DB 6; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
|||||||||||
Db 1 EGDFLAEGGGVR 12

RESULT 6
ADA18539
ID ADA18539 standard; peptide; 13 AA.
XX
AC ADA18539;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human alpha fibrinogen peptide #1.
XX
KW Alpha fibrinogen; human; myocardial infarction; SELDI; mass spectrometry;
KW surfaces enhanced for laser desorption/ionisation.
XX
OS Homo sapiens.
XX
PN US2002160422-A1.
XX
PD 31-OCT-2002.
XX
PF 30-APR-2001; 2001US-00846342.

XX
PR 30-APR-2001; 2001US-00846342.
XX
PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX
PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
DR WPI; 2003-219986/21.
XX
PT Novel biopolymer marker useful in indicating disease state, in particular
PT myocardial infarction.
XX
PS Disclosure; Fig 1; 10pp; English.
XX
CC The invention relates to a biopolymer marker useful in indicating at
CC least one particular disease state. This marker is characterised as alpha
CC fibrinogen having a molecular weight of 1077 Daltons and is useful for
CC indicating a disease state, in particular myocardial infarction. The
CC marker sequences are useful as antigens in immunoassays for the detection
CC of those individuals suffering from the disease known to be evidenced by
CC the marker sequence. The marker provides an efficient diagnostic tool for
CC rapidly and accurately diagnosing disease states such as myocardial
CC infarction. The marker was detected by the technique of surfaces enhanced
CC for laser desorption/ionisation (SELDI) mass spectroscopy. The present
CC sequence is the detected alpha fibrinogen marker peptide.
XX
SQ Sequence 13 AA;

Query Match 87.7%; Score 57; DB 6; Length 13;
Best Local Similarity 91.7%; Pred. No. 0.0055;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 1 EGDFLAEGGGVR 12

RESULT 7
ABU08827
ID ABU08827 standard; peptide; 14 AA.
XX
AC ABU08827;
XX
DT 25-AUG-2003 (first entry)
XX
DE Alpha fibrinogen peptide, #3, used for renal failure diagnostics.
XX
KW Proteomic; human; physiological condition; analyte; biopolymer;
KW biomarker; alpha fibrinogen; renal failure.
XX
OS Homo sapiens.
XX
PN US2002160420-A1.
XX
PD 31-OCT-2002.
XX
PF 30-APR-2001; 2001US-00846330.
XX
PR 30-APR-2001; 2001US-00846330.
XX
PA (JACK/) JACKOWSKI G.
PA (THAT/) THATCHER B.
PA (MARS/) MARSHALL J.
PA (YANT/) YANTHA J.
PA (VREE/) VREES T.
XX
PI Jackowski G, Thatcher B, Marshall J, Yantha J, Vrees T;
XX
DR WPI; 2003-491923/46.
XX
PT Determining proteomic basis e.g. basis for diagnosing existence of or
PT predicting development and/or progression of abnormal physiological
PT conditions based upon the presence of proteomic materials.
XX
PS Disclosure; Page 10; 25pp; English.
XX
CC The invention discloses a method for determining a proteomic basis for
CC development and progression of abnormal physiological conditions. The
CC method comprises isolating one or more patient specific proteomic
CC materials from a sample and comparing it against a library of proteomic
CC materials having characteristics identifiable with both normal and
CC abnormal physiological conditions or their predictive hallmarks. The
CC method is useful for determining a proteomic basis for development and
CC progression of abnormal physiological conditions. The method is also
CC useful for evaluating samples containing several analytes/biopolymers for
CC the presence of physiological condition specific sequences. The peptide
CC presented is a biomarker from alpha fibrinogen and is associated with
CC renal failure
XX
SQ Sequence 14 AA;

Query Match 87.7%; Score 57; DB 6; Length 14;
Best Local Similarity 91.7%; Pred. No. 0.006;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 2 EGDFLAEGGGVR 13

RESULT 8
AAR96194
ID AAR96194 standard; peptide; 16 AA.
XX
AC AAR96194;
XX
DT 19-DEC-1996 (first entry)
XX
DE Fibrinogen epitope probe, represents alpha chain residues 1-16.
XX
KW Epitope; cleavage product; human; leukocyte elastase; HLE; fibrinogen;
KW monoclonal antibody; probe; detection; antigen; blood; peritoneal fluid;
KW sputum; broncheoalveolar lavage fluid; assay; inhibitor; arthritis;
KW pulmonary emphysema; chronic bronchitis; cystic fibrosis; bronchiectasis;
KW chronic obstructive pulmonary disease; myelogenous leukaemia;
KW infantile respiratory distress syndrome; gout;
KW adult respiratory distress syndrome.
XX
OS Homo sapiens.
XX
PN WO9614580-A1.
XX
PD 17-MAY-1996.
XX
PF 03-NOV-1995; 95WO-US013794.
XX
PR 07-NOV-1994; 94US-00335524.
PR 06-JUN-1995; 95US-00469141.
XX
PA (MERI) MERCK & CO INC.
XX
PI Mumford RA, Davies DTP, Dahlgren ME, Boger JS, Humes JL;
XX
DR WPI; 1996-251888/25.
XX
PT New isolated fibrinogen derived cleavage products - used for detection of
PT leukocyte elastase activity in disease diagnosis and for evaluating
PT elastase inhibitors.
XX
PS Example 5; Page 42; 109pp; English.
XX
CC The sequences given in AAR96182-94 represent antigenic probes derived

CC from the first 21 amino acids of human fibrinogen. These probes are used
CC to determine antibody titre against other fibrinogen cleavage products.
CC The monospecific antibodies may be used to assay for the formation of
CC complimentary cleavage product antigens or epitopes in whole blood or
CC other body fluids, peritoneal fluid, sputum or broncheoalveolar lavage
CC fluid. The assay for cleavage products is dependent upon the presence of
CC HLE in the sample. This assay can also be used for the evaluation of HLE
CC inhibitors. The antibodies may be used to diagnose and monitor diseases
CC such as arthritis, gout, pulmonary emphysema, chronic bronchitis, cystic
CC fibrosis, chronic obstructive pulmonary disease, bronchiectasis, adult or
CC infantile respiratory distress syndrome and myelogenous leukaemia. See
CC also AAR96146-81
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 9
AAW04619
ID AAW04619 standard; peptide; 16 AA.
XX
AC AAW04619;
XX
DT 13-AUG-1997 (first entry)
XX
DE Fibrinopeptide A peptide for mass spectrometry analysis.
XX
KW Mass spectrometry; polymer analysis; biopolymer analysis.
XX
OS Synthetic.
XX
PN WO9636986-A1.
XX
PD 21-NOV-1996.
XX
PF 17-MAY-1996; 96WO-US007146.
XX
PR 19-MAY-1995; 95US-00446055.
PR 19-MAY-1995; 95US-00447175.
XX
PA (PERS-) PERSEPTIVE BIOSYSTEMS INC.
XX
PI Patterson DH, Tarr GE;
XX
DR WPI; 1997-012308/01.
XX
PT Sequencing polymers, e.g. DNA, RNA, peptide nucleic acids, proteins, etc.
PT - by obtaining mass to charge ratios of polymer fragments, pref. using
PT mass spectrometer, and performing statistical analysis.
XX
PS Example 2; Page 32; 86pp; English.
XX
CC A method of obtaining sequence information about a polymer (e.g. DNA,
CC RNA, peptide nucleic acids, proteins, peptides and carbohydrates)
CC comprising monomers of known mass has been claimed. The present sequence
CC represents a fibrinopeptide A peptide, and was used as an example as a
CC digestion before analysis by mass spectrometry, using this novel on-plate
CC strategy. Total sequence information from a nine well digestion can be
CC represented in a single digestion or it is often derived from two or more
CC wells. The methods, apparatus and kit (claimed) can be used for the
CC analysis of polymers, particularly biopolymers, e.g. DNA, RNA, peptide
CC nucleic acids, proteins, peptides and carbohydrates. It provides a rapid,
CC automated and cost effective sequencing of polymers, with a statistical
CC certainty
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 10
AAY57487
ID AAY57487 standard; peptide; 16 AA.
XX
AC AAY57487;
XX
DT 25-FEB-2000 (first entry)
XX
DE Antimicrobial peptide CS-FBP-alpha SEQ ID NO:25.
XX
KW Antimicrobial; metapeptide; PMP-2; platelet microbicidal protein;
KW antibiotic; infection; fungal; bacterial; neutrophil; apoptosis.
XX
OS Synthetic.
OS Oryctolagus cuniculus.
XX
PN WO9942119-A1.
XX
PD 26-AUG-1999.
XX
PF 17-FEB-1999; 99WO-US003350.
XX
PR 18-FEB-1998; 98US-00025319.
XX
PA (HARB-) HARBOR-UCLA RES & EDUCATION INST.
XX
PI Yeaman MR, Shen AJ;
XX
DR WPI; 1999-527417/44.
XX
PT Antimicrobial peptides for potentiating antimicrobial agents active
PT against bacteria and fungi.
XX
PS Disclosure; Page 120; 166pp; English.
XX
CC The present invention describes an antimicrobial peptide (AP) for direct
CC activity or for potentiating antimicrobial agents active against
CC organisms such as bacteria and fungi. The AP comprises: (a) a peptide
CC containing an amino acid sequence selected from the group consisting
CC essentially of a first peptide template XZBZBXBXB and its derivatives
CC selected from XZBBZBXBXB, BXZXB, BXZXZXB, XBBXZXBBX and BBXZBBXZ; and (b)
CC a second peptide template XBBXX and their derivatives selected from the
CC group consisting of XBBXBBX, XBBXXBBX, BXXBXXB, XBBZXXBB, and
CC XBBZXXBBXXZBBX; where B = at least one positively charged amino acid; X =
CC at least one non-polar hydrophobic amino acid; Z = at least one aromatic
CC amino acid, and where B, X and Z may be separated by one or more other
CC amino acids. The peptides can be used to treat bacterial and fungal
CC infections. The peptides also increase the antimicrobial activity of
CC neutrophils. The peptides overall effect cellular disruption and rapid
CC apoptosis of microbial cells. AAY57463 to AAY57557 represent sequences
CC used in the exemplification of the present invention
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 2; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 11
ABB56219
ID ABB56219 standard; peptide; 16 AA.
XX
AC ABB56219;
XX
DT 15-FEB-2002 (first entry)
XX
DE Vascular dementia-associated protein isoform (VPI) 419.
XX
KW Vascular Dementia; VD; VD-associated protein isoform; VPI; screening;
KW diagnosis; prognosis; gene therapy.
XX
OS Homo sapiens.
XX
PN WO200169261-A2.
XX
PD 20-SEP-2001.
XX
PF 14-MAR-2001; 2001WO-GB001106.
XX
PR 15-MAR-2000; 2000GB-00006285.
PR 24-NOV-2000; 2000GB-00028734.
PR 28-NOV-2000; 2000US-00724391.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2001-557937/62.
XX
PT Screening, diagnosis or prognosis of vascular dementia (VD), useful for
PT determining stage of VD and monitoring the effect of VD therapy,
PT comprises analyzing body fluid by 2-dimensional electrophoresis for
PT features correlated with VD.
XX
PS Claim 6; Page 39; 151pp; English.
XX
CC The invention relates to screening, diagnosis or prognosis of Vascular
CC Dementia (VD) in a subject comprising analysing body fluid from the
CC subject by 2-dimensional (2-D) electrophoresis to generate a 2-D array of
CC features containing at least one chosen feature whose relative abundance
CC correlates with the presence, absence, stage or severity of VD or
CC predicts the onset or course of VD, especially detecting in a sample of
CC cerebrospinal fluid (CSF) from the subject one of 223 VD-associated
CC protein isoforms (VPIs) (ABB55801-ABB56295) as fully defined in the
CC specification. Detecting VD-associated features and VPI is useful for the
CC screening, diagnosis or prognosis of VD, for determining the stage or
CC severity of VD, for identifying a subject at risk of VD or for monitoring
CC the effect of therapy administered to a subject having VD. Nucleic acids
CC encoding a VPI or inhibiting the function of a VPI are useful for the
CC treatment of VD and for gene therapy
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 4; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 12
AAB91959
ID AAB91959 standard; peptide; 16 AA.
XX
AC AAB91959;
XX
DT 22-JUN-2001 (first entry)
XX
DE Fibronectin fragment and fibrin related peptide SEQ ID NO:1135.
XX
KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
KW blood component; modification; succinimidyl; maleimido group; amino;
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200069900-A2.
XX
PD 23-NOV-2000.
XX
PF 17-MAY-2000; 2000WO-US013576.
XX
PR 17-MAY-1999; 99US-0134406P.
PR 10-SEP-1999; 99US-0153406P.
PR 15-OCT-1999; 99US-0159783P.
XX
PA (CONJ-) CONJUCHEM INC.
XX
PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;
XX
DR WPI; 2001-112059/12.
XX
PT Modifying and attaching therapeutic peptides to albumin prevents
PT peptidase degradation, useful for increasing length of in vivo activity.
XX
PS Disclosure; Page 567; 733pp; English.
XX
CC The present invention describes a modified therapeutic peptide (I)
CC comprising a therapeutically active amino acid region (III) and a
CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
CC a less therapeutically active amino acid region (IV), which covalently
CC bonds with amino/hydroxyl/thiol groups on blood components to form a
CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
CC factors and neurotransmitters, to protect them from peptidase activity in
CC vivo for the treatment of various disorders. Endogenous therapeutic
CC peptides are not suitable as drug candidates as they require frequent
CC administration due to rapid degradation by peptidases in the body.
CC Modifying and attaching therapeutic peptides to albumin prevents or
CC reduces the action of peptidases to increase length of activity (half
CC life) and specificity as bonding to large molecules decreases
CC intracellular uptake and interference with physiological processes.
CC AAB90829 to AAB92441 represent peptides which can be used in the
CC exemplification of the present invention
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 4; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 13
ABB52337
ID ABB52337 standard; peptide; 16 AA.
XX
AC ABB52337;
XX
DT 08-FEB-2002 (first entry)
XX
DE Human API-118 tryptic digest peptide #2.
XX
KW Human; neuroprotective; nootropic; gene therapy; vaccine;
KW Alzheimer's disease; Alzheimer's Disease-Associated Feature; AF;
KW Alzheimer's Disease-Associated Protein Isoform; API; tryptic digest;
KW Expression Reference Protein Isoform; ERPI; proteolysis.
XX

OS Homo sapiens.
XX
PN WO200175454-A2.
XX
PD 11-OCT-2001.
XX
PF 03-APR-2001; 2001WO-US010908.
XX
PR 03-APR-2000; 2000US-0194504P.
PR 28-NOV-2000; 2000US-0253647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
PA (PFIZ) PFIZER INC.
XX
PI Durham KL, Friedman DL, Herath HMAC, Kimmel LH, Parekh RB;
PI Potter DM, Rohlff C, Silber BM, Stiger TR, Sunderland PT;
PI Townsend RR, White F, Williams SA;
XX
DR WPI; 2001-639384/73.
XX
PT Screening for Alzheimer's disease in a mammal, by making two-dimensional
PT array of a feature whose relative abundance correlates with disease, and
PT comparing with abundance of the feature in samples of healthy persons.
XX
PS Example; Page 33; 162pp; English.
XX
CC The invention relates to methods for the screening, diagnosis and
CC prognosis of Alzheimer's disease. The methods involve the detection of
CC Alzheimer's Disease-Associated Features (AFs) and Alzheimer's Disease-
CC Associated Protein Isoforms (APIs) in cerebrospinal fluid, serum or
CC plasma. The abundance of the AFs and APIs is then normalised to an
CC Expression Reference Protein Isoform (ERPI) in order to determine whether
CC a patient is suffering from, or has a predisposition to, Alzheimer's
CC Disease. The relative abundance of the AFs and APIs correlates with the
CC severity of Alzheimer's Disease. The present sequence is a peptide
CC produced from an API by proteolysis
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 4; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 14
ABG73668
ID ABG73668 standard; peptide; 16 AA.
XX
AC ABG73668;
XX
DT 11-MAR-2003 (first entry)
XX
DE Linear HIV-1 gp120 V3-loop derived peptide ligand SEQ ID 11.
XX
KW gp120; interaction; co-receptor; CXCR4; CCR5; refractive index; V3 loop;
KW 7-helix transmembrane receptor; glycopeptide; virucide; anti-HIV;
KW HIV infection.
XX
OS Human immunodeficiency virus 1.
OS Synthetic.
XX
PN DE10113042-A1.
XX
PD 26-SEP-2002.
XX
PF 09-MAR-2001; 2001DE-01013042.
XX
PR 09-MAR-2001; 2001DE-01013042.
XX
PA (NOCH-) NOCHT INST TROPENMEDIZIN BERNHARD.
XX
PI Schreiber M, Seifert A, Meyer B;
XX
DR WPI; 2002-752120/82.
XX
PT Identifying compounds that modify interaction of gp120 and co-receptors,
PT useful potentially for treating human immune deficiency virus infection,
PT also new peptides.
XX
PS Claim 10; Page 56; 68pp; German.
XX
CC This invention describes novel substances that modify the interaction
CC between the gp120 protein of human immunodeficiency virus (HIV), or its
CC fragments, with the co-receptors CXCR4, CCR5 and/or other 7-helix
CC transmembrane receptors for HIV. The method comprises (a) immobilizing a
CC ligand for the co-receptor on a gold surface; (b) contacting the ligand
CC with suspended cells that express the co-receptor; and (c) determining
CC interaction by measuring the refractive index (RI) by plasmon resonance.
CC The procedure is repeated using cells that have been incubated with a
CC test compound, and this is identified if RI is lower for cells
CC preincubated with it. The ligand is a linear or cyclic (glyco)peptide
CC that includes the amino acid sequence of an HIV V3 loop (including
CC flanking Cys). The products of the invention have virucide and anti-HIV
CC (human immunodeficiency virus) activity and are useful for prevention
CC and/or treatment of HIV infection. This sequence represents a linear HIV-
CC 1 gp120 V3-loop derived peptide ligand described in the disclosure of the
CC invention
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 5; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ESDFLAEGGGVR 13
| ||||||||||
Db 5 EGDFLAEGGGVR 16

RESULT 15
ABG78799
ID ABG78799 standard; peptide; 16 AA.
XX
AC ABG78799;
XX
DT 29-NOV-2002 (first entry)
XX
DE Multiple sclerosis associated feature (MSF) tryptic digest peptide #287.
XX
KW Multiple sclerosis; MS; multiple sclerosis associated feature; MSAF;
KW human; multiple sclerosis-associated protein isoform; MSPI;
KW antiinflammatory; neuroprotective.
XX
OS Homo sapiens.
XX
PN WO200259604-A2.
XX
PD 01-AUG-2002.
XX
PF 25-JAN-2002; 2002WO-GB000330.
XX
PR 26-JAN-2001; 2001US-0264404P.
PR 20-NOV-2001; 2001US-0331647P.
XX
PA (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
XX
PI Herath HMAC, Parekh RB, Rohlff C;
XX
DR WPI; 2002-599812/64.
XX
PT Screening or diagnosing multiple sclerosis (MS), useful for e.g.
PT determining the stage or severity of MS, comprises detecting the presence

PT of MS-associated features or protein isoforms by 2-dimensional
PT electrophoresis.
XX
PS Disclosure; Page 32; 128pp; English.
XX
CC This invention relates to a novel method for screening or diagnosing
CC multiple sclerosis (MS) in a subject to determine the stage or severity
CC of MS, to identify a subject at risk of developing MS or to monitor the
CC effect of a therapy administered. The method comprises analysing a sample
CC body fluid from the subject by two-dimensional electrophoresis and
CC detecting the presence of multiple sclerosis-associated features (MSFs),
CC or multiple sclerosis-associated protein isoforms (MSPIs). The MSF's of
CC the invention correspond to spots identified on a 2D gel these proteins
CC may have antiinflammatory or neuroprotective activity. The methods of the
CC invention and the compositions are useful for clinical screening,
CC diagnosis and treatment of MS, for monitoring the effectiveness of MS
CC treatment, for selecting participants in clinical trials, for identifying
CC patients most likely to respond to a particular therapeutic treatment and
CC for screening and developing drugs for treatment of MS. Agents that
CC modulate the expression or activity of an MSPI are useful for treating
CC MS, for preventing or delaying the onset or development of MS, to prevent
CC or delay the progression of MS, or to ameliorate the symptoms MS. Nucleic
CC acids comprising a sequence encoding an MSPI, MSPI-related polypeptide,
CC or their fragments are useful for promoting MSPI function by gene
CC therapy. The present sequence represents a human multiple sclerosis
CC associated feature tryptic digest peptide of the invention
XX
SQ Sequence 16 AA;

Query Match 87.7%; Score 57; DB 5; Length 16;
Best Local Similarity 91.7%; Pred. No. 0.0069;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 ESDFLAEGGGVR 13
              | ||||||||||
Db          5 EGDFLAEGGGVR 16
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